

DRAWINGS

Fig. 1

9 18 27 36 45 54

5' GTG GGC ATG GTG GGC AAC GTC CTG CTG GTG CTG GTG ATC GCG CGG CGG CGG CGG
 Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg

63 72 81 90 99 108

CTG CAC AAC GTG ACG AAC TTC CTC ATC GGC AAC CTG GCC TTG TCC GAC GTG CTC
 Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu

117 126 135 144 153 162

ATG TGC ACC GCC TGC GTG CCG CTC ACG CTG GCC TAT GCC TTC GAG CCA CGC GGC
 Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly

171 180 189 198 207 216

TGG GTG TTC GGC GGC CTG TGC CAC CTG GTC TTC TTG CTG CAG CCG GTC ACC
 Trp Val Phe Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr

225 234 243 252 261 270

GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GCA GTG GAC CGG TAC GTC GTG
 Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val Val

279 288 297

CTG GTG CAC CCG CTG AGG CGG CGC ATC 3'

Leu Val His Pro Leu Arg Arg Arg Ile

Fig. 2

9	18	27	36	45	54
5' GGC CTG CTG CTG GTC ACC TAC CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC					
Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr					

63	72	81	90	99	108
GTC CGG GTG TCA GTG AAG CTC CGC AAC CGC GTG GTG CCG GGC TGC GTG ACC CAG					
Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Cys Val Thr Gln					

117	126	135	144	153	162
AGC CAG GCC GAC TGG GAC CGC GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG GTG					
Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Thr Phe Cys Leu Leu Val					

171	180	189	198		
GTG GTC GTG GTG GTG TTT GCC ATC TGC TGG TTG CCT TAC TAC 3'					
Val Val Val Val Val Phe Ala Ile Cys Trp Leu Pro Tyr Tyr					

Fig. 3

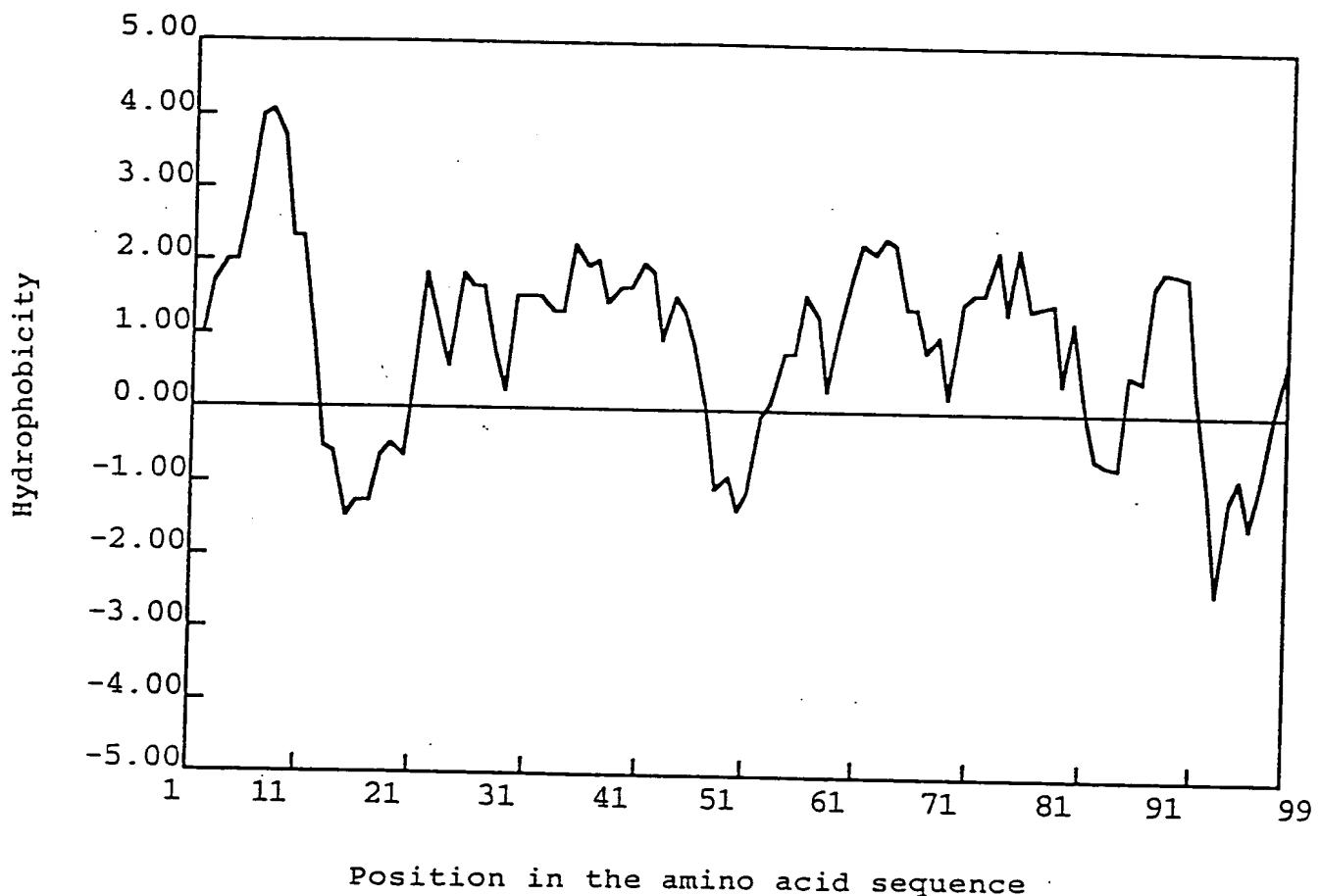


Fig. 4

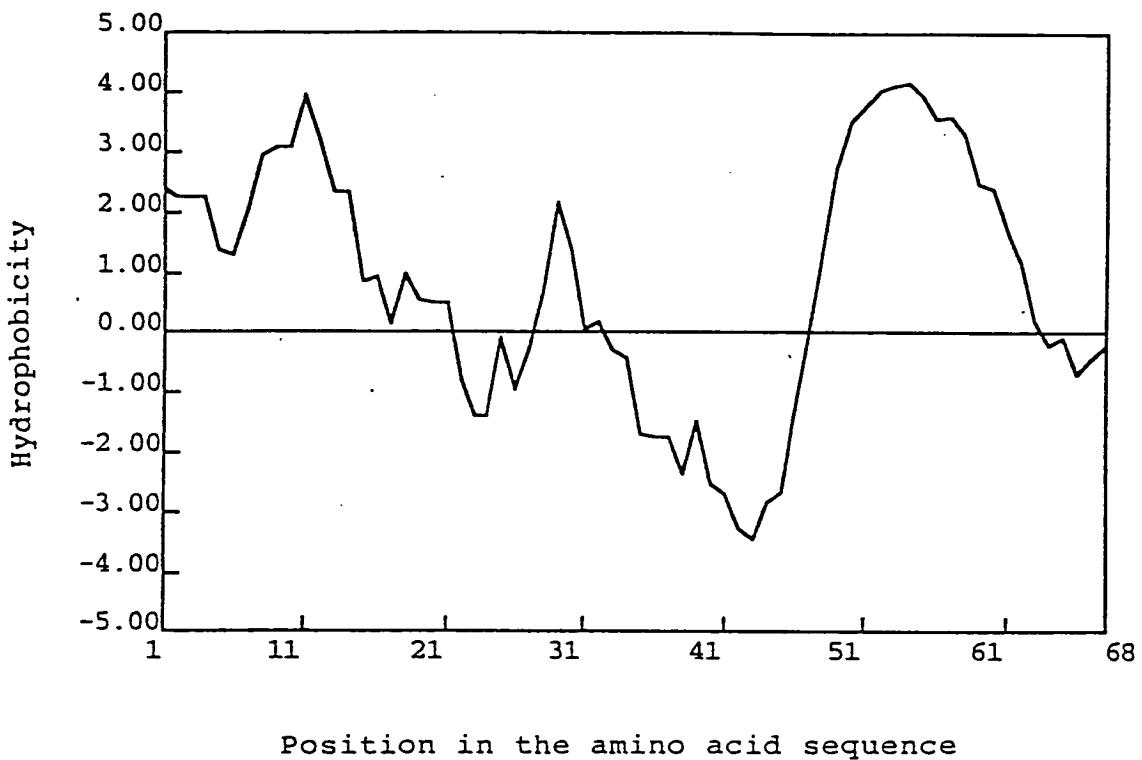


Fig. 5

10 20 30 40 50
1 VGVGNVLFV LVFARVRLH NVTNF LIGNL ALSDVIMCTA CVPLTAYAF
1 LGVSGNLLRI IIIKQKEMR NVTNLLIVNL SFSDLKAVM CLPFTVYTL
50 50

p19P2 10 20 30 40 50
S12863 1 VGVGNVLFV LVFARVRLH NVTNF LIGNL ALSDVIMCTA CVPLTAYAF
1 LGVSGNLLRI IIIKQKEMR NVTNLLIVNL SFSDLKAVM CLPFTVYTL
50 50

p19P2 60 70 80 90 100
S12863 51 ERGWMWEGEG LCHLVFELQP ViryVSVFEL TTIAVDRVV LVHPLRRRI-
51 MDH-WVFGET MCKLNPEVQC VSITVSIEST VLTAVERHQL IINPRGWPN
100 100

p19P2 110 120 130 140 150
S12863 101 -----
101 NRHAYIGITY IIVIHAVASSL PFVITYQILID EPFQNVSLAA FKDKYVCFDK
150 150

p19P2 160 170 180 190 200
S12863 151 ----GLV TYTPLVIL LS-----Y VRVSVK DNR VVPGCVTQSQ
151 FPSDSHRLSY TRLLVQXF GPLCFIFICY FKIYIR KRR NNIMMDKIRD
200 200

p19P2 210 220 230 240 250
S12863 201 ADMDRARR RR TFC LEVWV VFAICMLPYY
201 KYRSSETKRI NMMLISIWA -FAVCMLPUT
250 250

Fig. 6

9 18 27 36 45 54

5' GTG GGC ATG GTG CCC AAC ATC CTG CTG GTG ATC GCG CGG GTG CGC CGG
--- --- --- --- --- --- Val Gly Met Val Gly Asn Ile Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg

63 72 81 90 99 108

CTG TAC AAC GTG ACG AAT TTC CTC ATC GGC AAC CTG GCC TTG TCC GAC GTG CTC
--- --- --- --- --- --- Leu Tyr Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu

117 126 135 144 153 162

ATG TGC ACC GGC TGC GTG CCG CTC ACG CTG CCC TAT GCC TTC GAG CCA CGC GGC
--- --- --- --- --- --- Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly

171 180 189 198 207 216

TGG GTG TTC GGC GGC CTG TGC CAC CTG GTC TTC CTG CAG GCG GTC ACC
--- --- --- --- --- --- Trp Val Phe Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr

225 234 243 252 261 270

GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GCA GTG GAC CGC TAC GTC GTG
--- --- --- --- --- --- Val Tyr Val Ser Val Phe Thr Leu Thr Ile Ala Val Asp Arg Tyr Val Val

279 288 297 306 315 324

CTG GTG CAC CCG CTG AGG CGG CGC ATC TCG CTG CGC CTC AGC GCC TAC GCT GTG
--- --- --- --- --- --- Leu Val His Pro Leu Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val

333 342 351 360 369 378

CTG GCC ATC TGG GTG CTG TCC GCG GTG CTG GCG CTG CCC GCC GCC GTG CAC ACC
--- --- --- --- --- --- Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr

387 396 405 414 423 432

TAT CAC GTG GAG CTC AAG CCG CAC GAC GTG CGC CTC TCC GAG GAG TTC TGG GGC
--- --- --- --- --- --- Tyr His Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly

441 450 459 468 477 486

TCC CAG GAG CGC CAG CGC CAG CTC TAC GCC TGG GGG CTG CTG GTC ACC TAC
--- --- --- --- --- --- Ser Gln Glu Arg Gln Leu Tyr Ala Trp Gly Leu Leu Val Thr Tyr

495 504 513 522 531 540

CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC GCC CCG GTG TCA GTG AAG CTC
--- --- --- --- --- --- Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu

549 558 567 576 585 594

CGC AAC CGC GTG CCG GGC CGC GTG ACC CAG AGC CAG GCC GAC TGG GAC CGC
--- --- --- --- --- --- Arg Asn Arg Val Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg

603 612 621 630 639 648

CCT CGG CGC CGG CCC ACC TTC TGC TTG CTG GTG GTC GTG GTG GTG TTC ACC
--- --- --- --- --- --- Ala Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Thr

657 666

CTC TCC TGG CTG CCC TTC TTC
--- --- --- --- --- Leu Cys Trp Leu Pro Phe Phe

Fig. 7

p19P2		10	VGMVGNVLLV	LVIARVRLH	NVTNFLIGNL	ALSDVLMCTA	CVFILAYAF	50
PG3-2/pG1-10	1	1	VGMVGNVLLV	LVIARVRLY	NVTNFLIGNL	ALSDVLMCTA	CVPILAYAF	50
p19P2		60	EPRGMVFGGG	LCHLMEFLQP	VTYYVSVFYL	TIAVDRVV	LVHPLRRRI-	100
PG3-2/pG1-10	51	51	EPRGMVFGGG	LCHLMEFLQA	VTYYVSVFYL	TIAVDRVV	LVHPLRRRIS	100
p19P2		110	-----	120	130	140	150	-----
PG3-2/pG1-10	101	101	-----	-----	-----	-----	-----	150
p19P2		160	GILLV	TYLLPLVL	LSYVRVSVKL	RNRVVPGRVT	QSQADMDRAR	200
PG3-2/pG1-10	151	151	QLYAWGLLV	TYLLPLVL	LSYVRVSVKL	RNRVVPGRVT	QSQADMDRAR	200
p19P2		210	RRRTFCLLW	WVVEAIICML	PYY	230	240	250
PG3-2/pG1-10	201	201	RRRTFCLLW	WVVEAIICML	PEF	250
						250

Fig. 8

Hydrophobicity

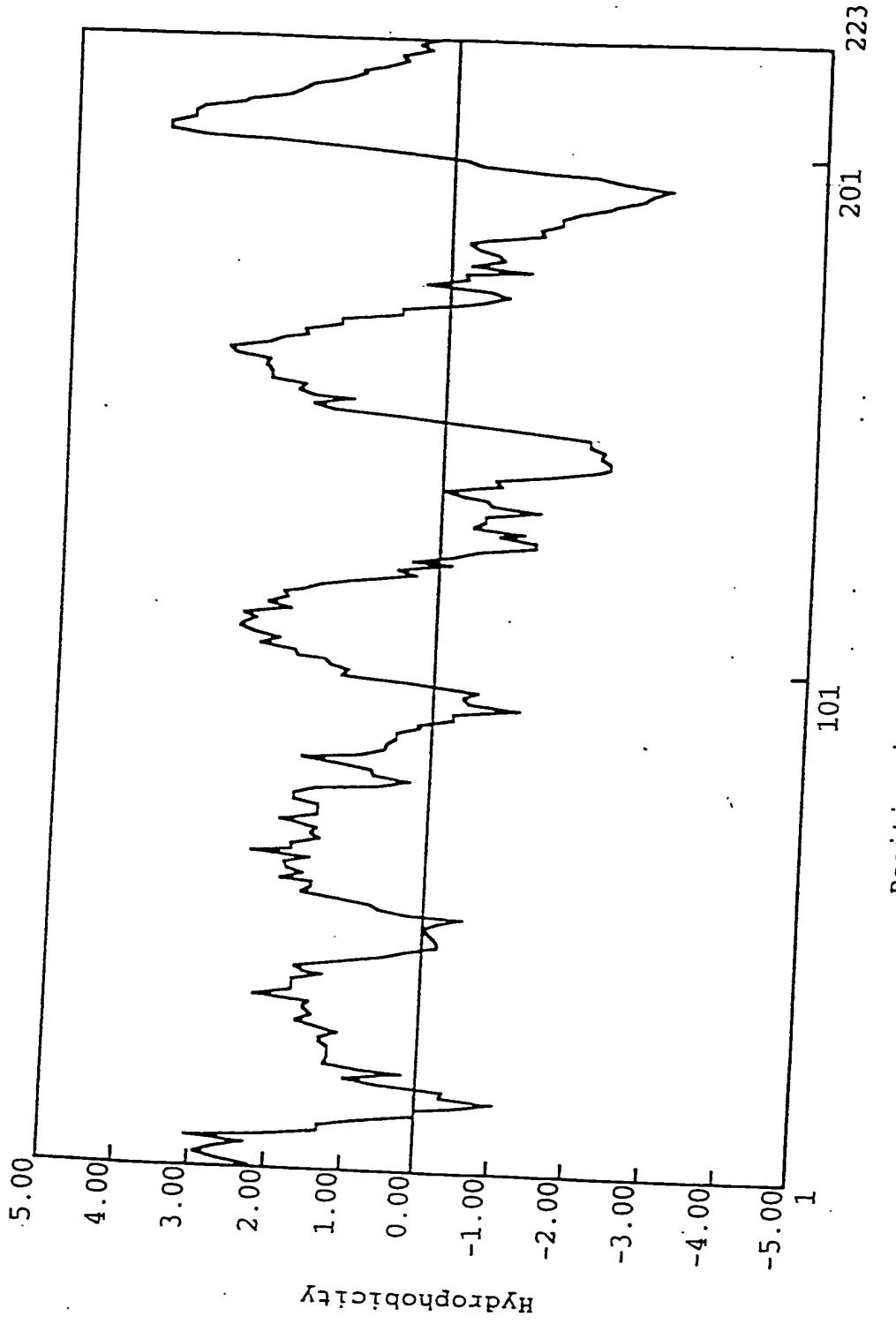


Fig. 9

1	CATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCGAGGCCAGCAGAAATT	60
1		1
61	CTGCCCCCTTCTTCCCAGGACTGCTTTCGGCTCTCCAAACCCCACTCCAGGTGGCCATG	120
1		1
121	GCCTCATCGACCCTCGGGGCCCCAGGGTTCTGACTTATTTCTGGGCTGCCGCCGGCG	180
1	AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla	21
181	GTCACAACTCCGCCAACAGAGGCCAGAGGCTCGGCCGGCAACGGGTCGGTGGCTGGC	240
21	ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly	41
241	GCGGACGCTCCAGCGTACGCCCTTCCAGGGCTGCACTGGTGCATCAGCTGAAGGGG	300
41	AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly	61
301	CTGATCGTGTGCTCTACAGCGTCGGTGGCTGGTGGCTGGTGGCAACTGCCTGCTG	360
61	LeuIleValLeuLeuTyrSerValValValValGlyLeuValGlyAsnCysLeuLeu	81
361	CTGGCTGGTGATCGCGGGGTGCGCCGGCTGCACACGTGACGAACCTCTCATCGGCAAC	420
81	ValLeuValIleAlaArgValArgArgLeuHisAsnValThrAsnPheLeuIleGlyAsn	101
421	CTGGCCTTGTCCGACGTGCTCATGTGCAACGCCCTGCGTGCCTCACGCTGGCTATGCC	480
101	LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla	121
481	TTCGAGCCACCGGGCTGGGTTCTGGCTGGCGGGCTGTGCCACCTGGCTTCTCTCTGAG	540
121	PheGluProArgGlyTrpValPheGlyGlyLeuCysHisLeuValPhePheLeuGln	141
541	CCGGTCACCGCTATGTGTCGGTTCACGCTCACCACTCGCAGTGGACCGCTACGTC	600
141	ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal	161
601	GTGCTGGTGCACCCGCTGAGCGGGCCATCTCGCTGCGCCTACGGCCTACGCTGTGCTG	660
161	ValLeuValHisProLeuArgArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu	181
661	GCCATCTGGCGCTGTCGGCTGCGCCGCTGCCGCGCCGCTGCACACCTATCACGTG	720
181	AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal	201
721	GAGCTCAAGCCGACGACGTGCGCCTCTGGAGGGAGTTCTGGGCTCCAGGAGGCCAG	780
201	GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln	221
781	CGCCAGCTCACGCCCTGGGGCTGCTGGTCACCTACCTGCTCCCTGCTGGTCATC	840
221	ArgGlnLeuTyrAlaTrpGlyLeuLeuValThrTyrLeuLeuProLeuLeuValIle	241
841	CTCCGTCTTACGTCCGGTGTCACTGAAGCTCCGCAACCGCGTGGTGCCTGGCTGGTG	900
241	LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal	261
901	ACCCAGAGCCACGGCCGACTGGGACCGCCGCTGGCGCCGGCACCTCTGCTGGCTGGTG	960
261	ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgArgThrPheCysLeuLeuVal	281
961	GTGGCTGGTGGTGTCTGGCTGCGCTGCGCTGCACGTCTTCAACCTGCTGGCG	1020
281	ValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg	301
1021	GACCTCGACCCCCACGCCATCGACCCCTACGCCCTGGGCTGGTCAGCTGCTCTGCCAC	1080
301	AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis	321
1081	TGGCTGCCATGAGTTGGCTGCTACAACCCCTCATCTACGCCCTGGCTGCACGACAGC	1140
321	TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer	341
1141	TTCCGGAGGAGCTGGCAAACGTGTTGGTCGCTGGCCCCGCAAGATAGCCCCCATGGC	1200
341	PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly	361
1201	CAGAATATGACCGTCAGCGTGGTCATCTGATGCCACTTAGCCAGGCCCTGGTCAAGGACC	1260
361	GlnAsnMetThrValSerValValIle...	371
1261	TCCACTTCAACTGGCCTCTACGCCACCACTGGCTCAATCTGGCTTATTCTCAGCA	1320
371		371
1321	CCAGAGCTAGC	1331
371		371

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Fig. 10

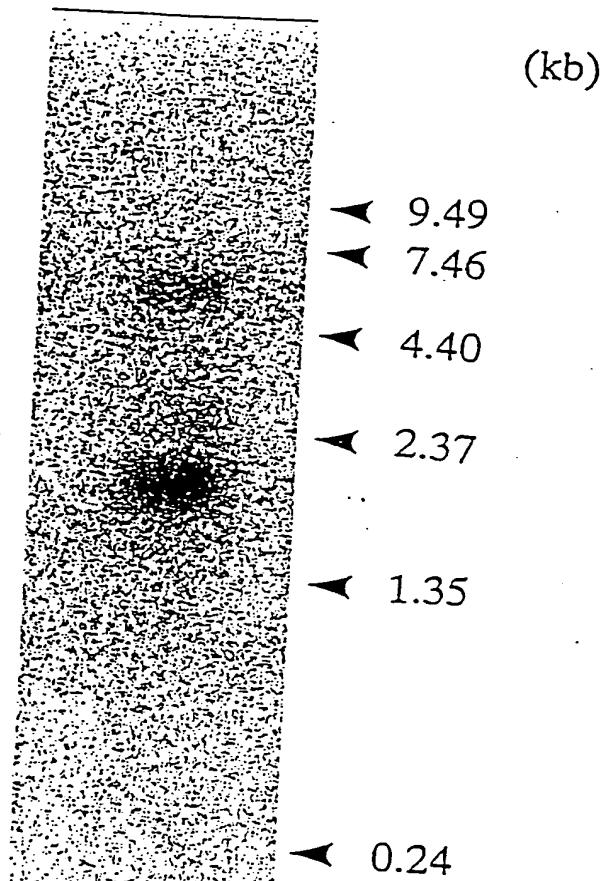


Fig. 11

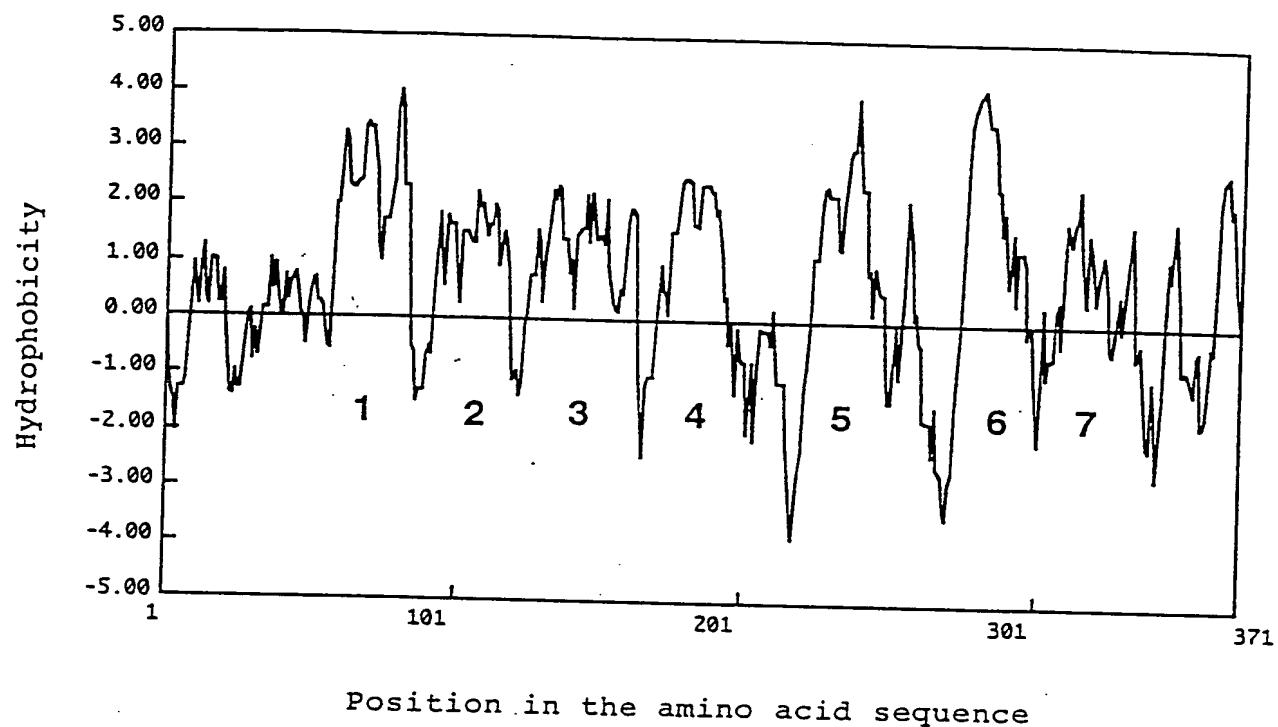


Fig. 12

5' 9 18 27 36 45 54
 CTG TGT GTC ATC GCG GTG GAT AGG TAC GTG GTT CTG GTG CAC CCG CTA CGT CGG
Leu Cys Val Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg Arg
 63 72 81 90 99 108
 CGC ATT TCA CTG AGG CTC AGC GCC TAC GCG GTG CTG GCC ATC TGG GCT CTA TCT
Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser
 117 126 135 144 153 162
 GCA GTG CTG GCG CTG CCG GCC GCG GTG CAC ACC TAC CAT GTG GAG CTC AAG CCC
Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro
 171 180 189 198 207 216
 CAC GAC GTG AGC CTC TGC GAG GAG TTC TGG GGC TCG CAG GAG CGC CAA CGC CAG
His Asp Val Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln
 225 234 243 252 261 270
 ATC TAC GCC TGG GGG CTG CTT CTG GGC ACC TAT TTG CTC CCC CTG CTG GCC ATC
Ile Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala Ile
 279 288 297 306 315 324
 CTC CTG TCT TAC GTA CGG GTG TCA GTG AAG CTG AGG AAC CGC GTG GTG CCT GGC
Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly
 333 342 351 360 369 378
 AGC GTG ACC CAG AGT CAA GCT GAC TGG GAC CGA GCG CGT CGC CGC CGC ACT TTC
Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe
 387 396 405 414 423 432
 TGT CTG CTG GTG GTG GTG GTA GTG TTC ACG CTC TGC TGG CTG CCC TTC TAC
Cys Leu Leu Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Tyr

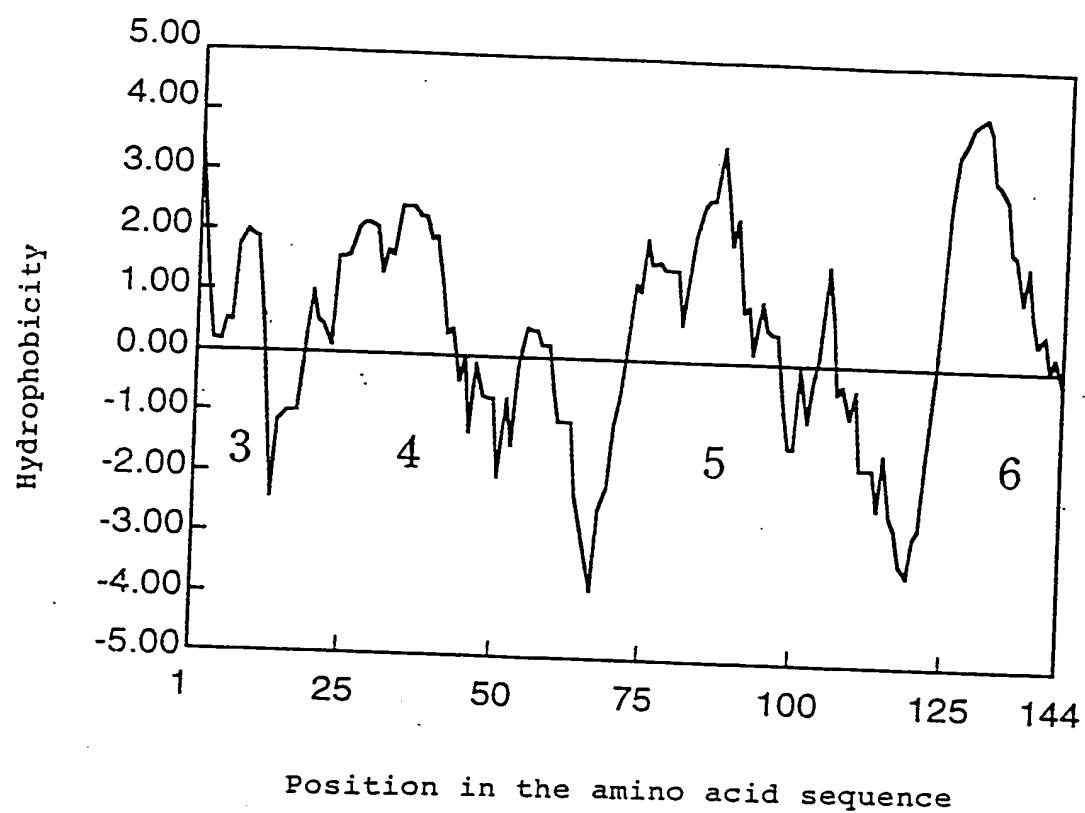
CT 3'

--

Fig. 13

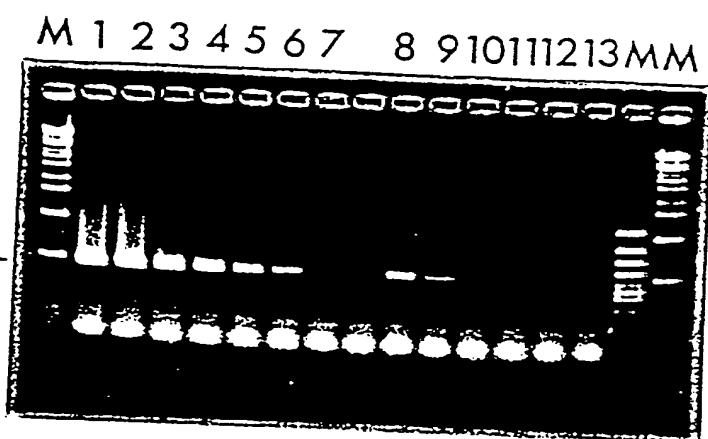
the first time he had seen her, he had been struck by her beauty.

Fig. 14



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Fig. 15



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Fig. 16

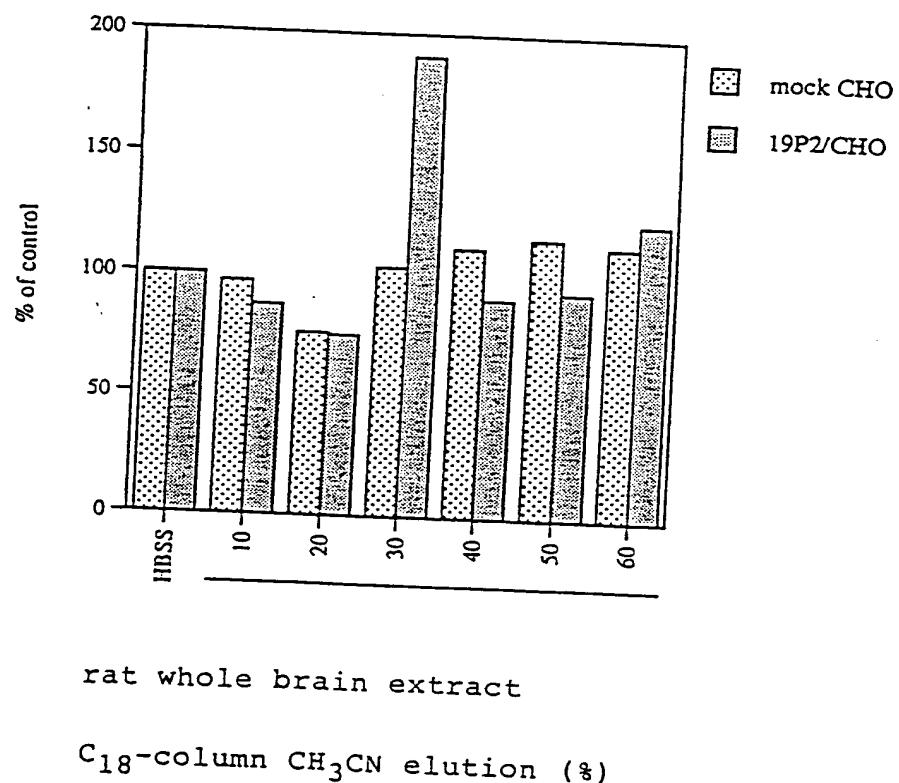


Fig. 17

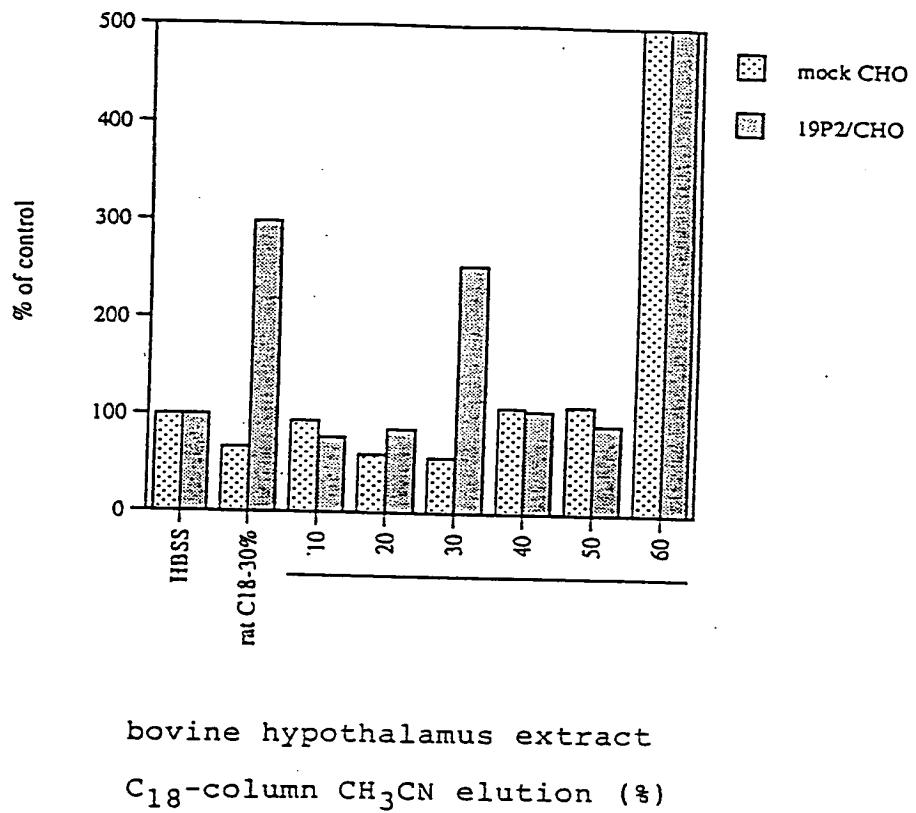


Fig. 18



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Fig. 19

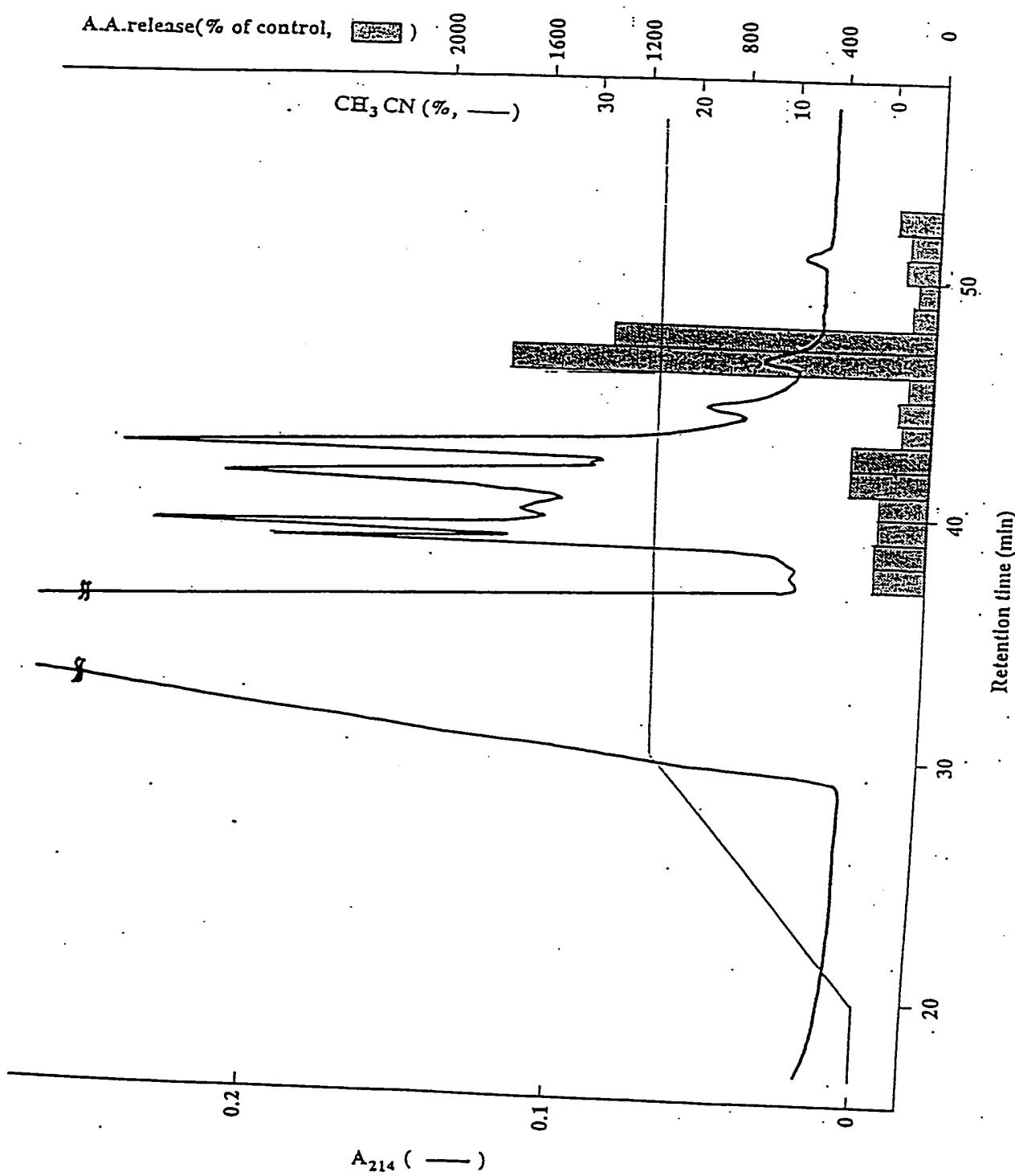
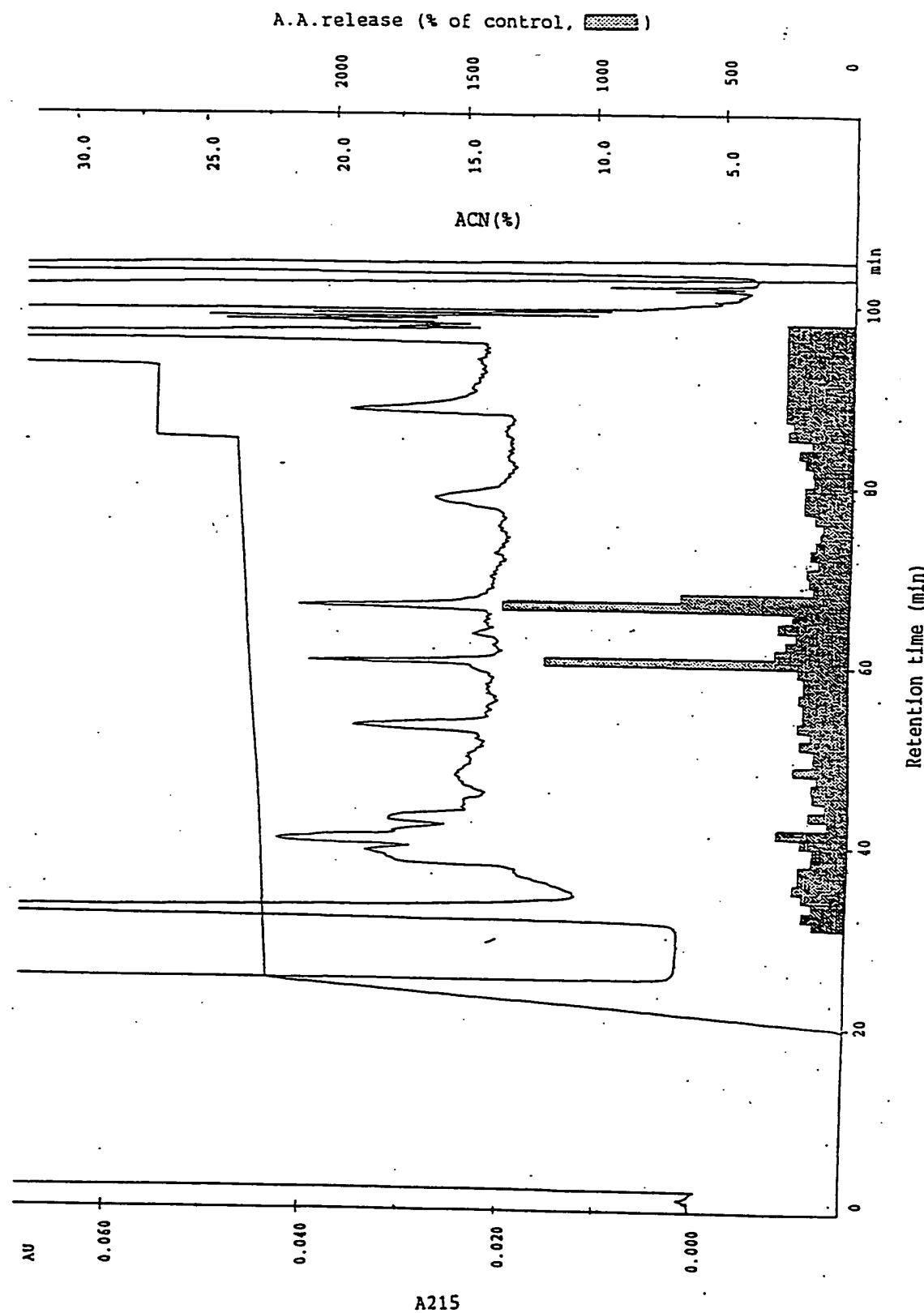


Fig. 20



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Fig. 21

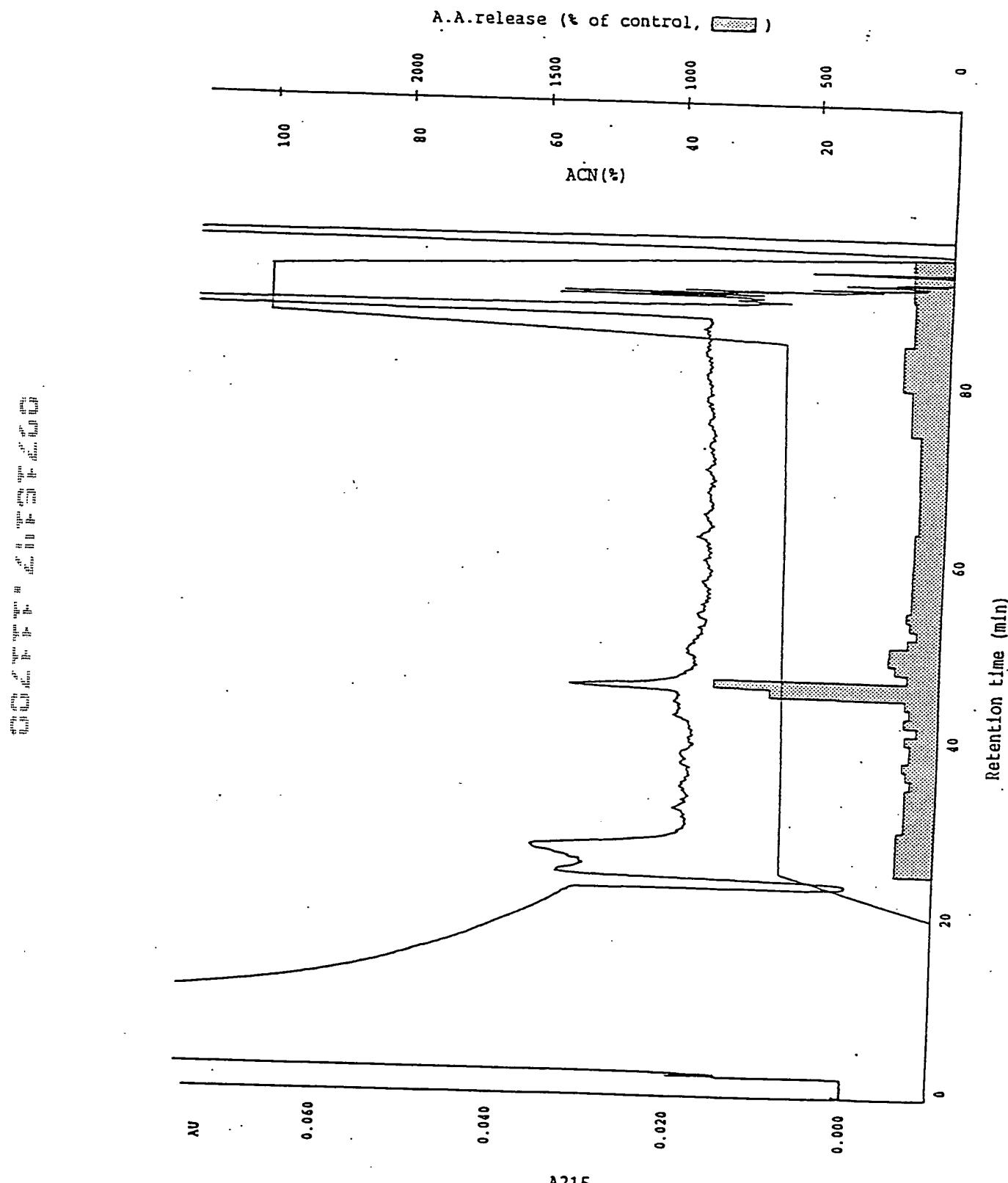


Fig. 22

P5-1

5' 9 18 27 36 45 54
 GCC CAC CAG CAC TCC ATG GAG ATC CGC ACC CCC GAC ATC AAC CCT GCC TGG TAC

 Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr
 63 72
 GCG GGC CGT GGG ATC CGG CCC G 3'

 Ala Gly Arg Gly Ile Arg Pro

P3-2

Fig. 23

1	GTGGAATGAAGCGGTGGGGCCTGGCTCCTCTGCCTGCTGCTGGCCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
	PDN	
120	CCTGCCT	126
39	<u>ProAla</u>	40

Fig. 24 (a)

1	GTGGAATGAAGCGGTGGGGCCTGGCTCCTGCCTGCTGCTGGCCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGGCTGCC <u>AGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC</u>	119
19	GlnGlyAlaAla <u>SerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn</u>	38
120	<u>CCTGCCTGGTACGCRRGGCGTGGGATCCGGCCCGTGGGC</u> CGCTTCGGCCGGCGAAGAGCT	179
39	<u>ProAlaTrpTyrAlaGlyArgGlyIleArgProValGly</u> ArgPheGlyArgArgArgAla	58
180	GCCCCGGGGGACGGACCCAGGCCTGGCCCCCGGCGTGTGCGGGCCTGCTTCCGCCTGGAA	239
59	AlaProGlyAspGlyProArgProGlyProArgArgValProAlaCysPheArgLeuGlu	78
240	GGCGGYGCTGACCCCTCCGAGCCCTCCGGGGCGGCTGACGGCCAGCTGGTCCAGGAA	299
79	GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu	98
300	TAACAGCGGGAGCCTGCCCTCCCCACCCCTCCTCCACCAGCCACCTCCCTCCAGTCCT	359
98		98
360	AATAAAAGCAGCTGGCTTGTT	380
98		98

Fig. 24 (b)

1	GTGGAATGAAGGCGGTGGGGCCTGGCTCCTCTGCCTGCTGCTGGCCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGGCTGCC <u>AGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC</u>	119
19	GlnGlyAlaAla <u>SerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn</u>	38
120	<u>CCTGCCTGGTACCGCRGGCCGTGGGATCCGGCCCGTGGGCGCTTCGGCCGGCGAAGAGCT</u>	179
39	<u>ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgArgAla</u>	58
180	GCCCTGGGGACGGACCCAGGCCTGGCCCCCGCGTGTGCGCCCTGCTTCCGCCTGGAA	239
59	AlaLeuGlyAspGlyProArgProGlyProArgArgValProAlaCysPheArgLeuGlu	78
240	GGCGGYGCTGAGCCCTCCGAGCCCTCCGGGGCGGCTGACGGCCAGCTGGTCCAGGAA	299
79	GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu	98
300	TAACAGCGGGAGCCTGCCCTACCCCTCCTCCACCAGCCACCTCCAGTCCT	359
98		98
360	AATAAAAGCAGCTGGCTTGT	380
98		98

Fig. 25

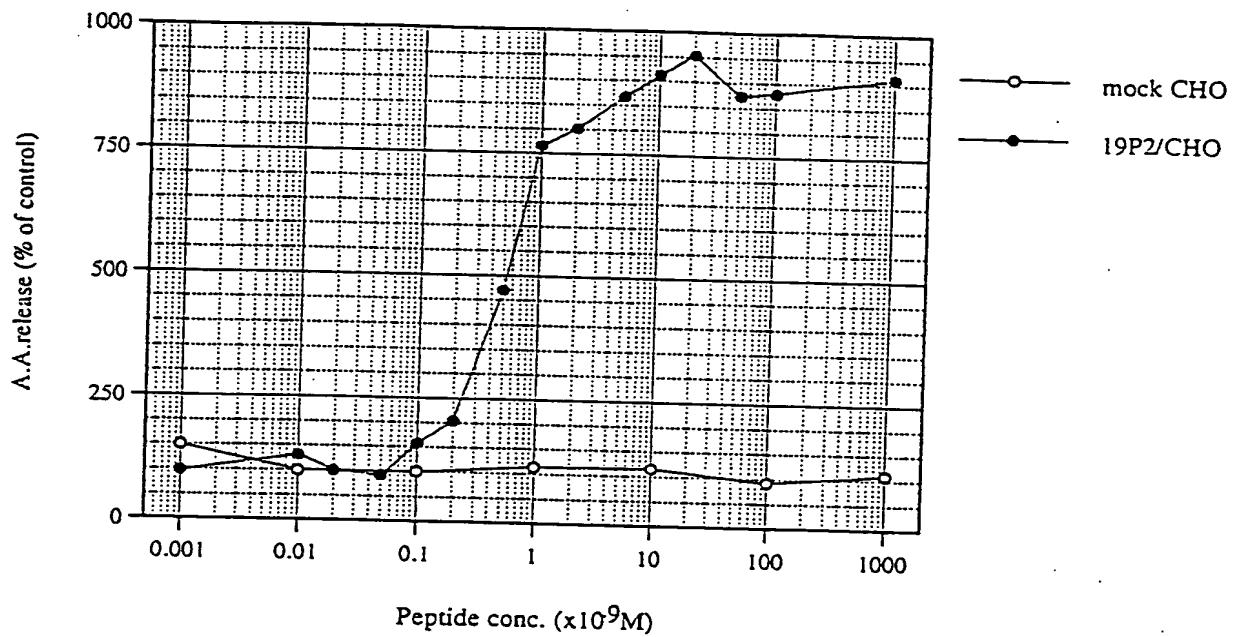


Fig. 26

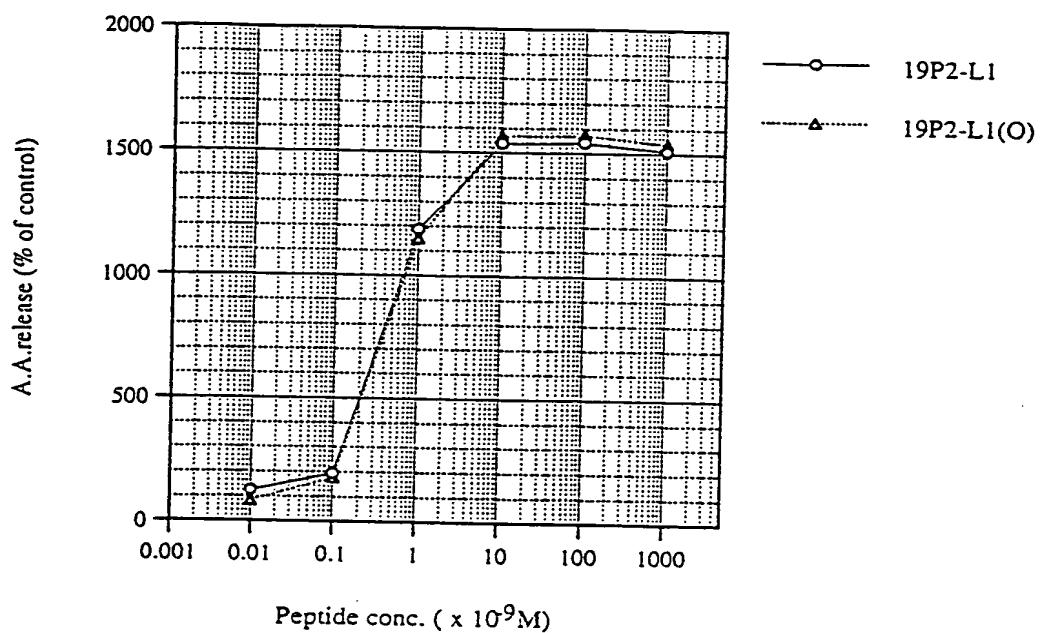
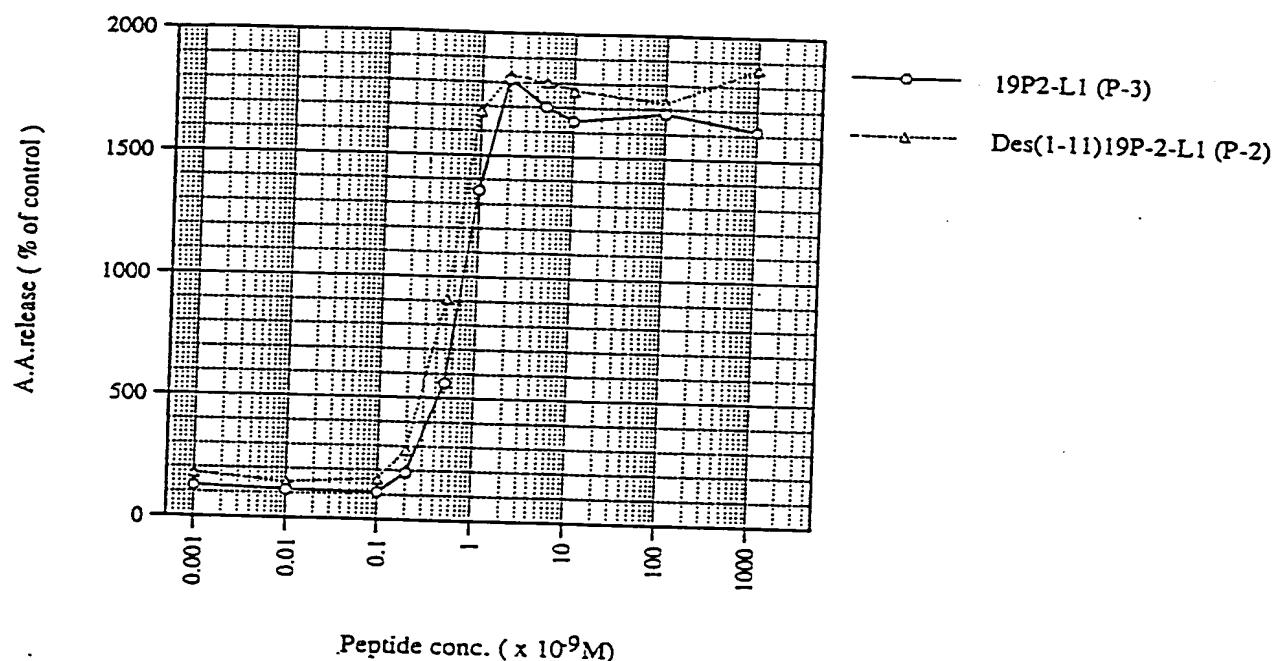


Fig. 27



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Fig. 28

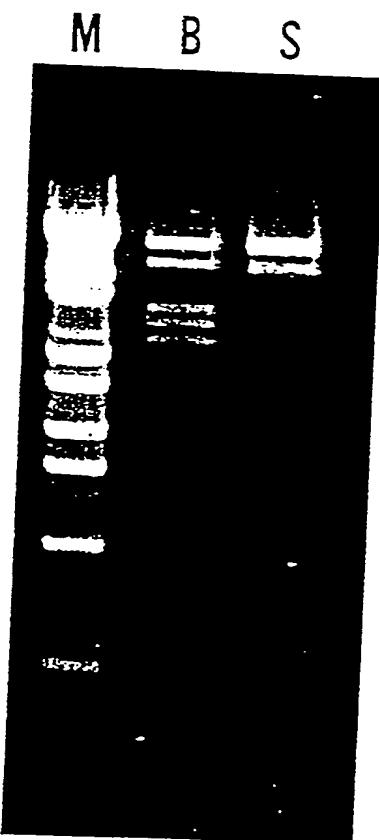


Fig. 29

10	20	30	40	50	60
ATGAAGCCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG
70	80	90	100	110	120
GCTGCCAGCA	GAGCCCACCA	GCACCTCCATG	GAGATCCGCA	GTGAGTGTCT	AGCCCCCGCC
130	140	150	160	170	180
CTGCCCCCAG	GGGTCACAGG	GGGGGCCTGG	CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA
190	200	210	220	230	240
GCATCCTGGG	GTTGGGGTTT	GGCCTCCTGT	TCCCCAGACC	CITCCCCCAG	GTGGCCCGGA
250	260	270	280	290	300
CAGGTGCTCC	CAAGGGTCCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACCTCCTC	ACCACACGGG
310	320	330	340	350	360
TGGCCTGGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	GGAAAGGAAG
370	380	390	400	410	420
GGGAGTGTGT	CCTGGTGTGA	CTCTGAATC	CTACTTCCCA	AAGCCACCCC	AGCACCAAGAA
430	440	450	460	470	480
ATGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA
490	500	510	520	530	540
GGCAGCCATG	AGCTGAGCAC	ACACCCGGCC	CGGCCACCAAG	GGCTGTATGC	TCCAGGGCAC
550	560	570	580	590	600
AGGCCTCCAT	GCGCTTTCT	CTCTCTTCC	AGCCCCCGAC	ATCAACCTG	CCTGGTACGC
610	620	630	640	650	660
AGGCCGTGGG	ATCCGGCCCG	TGGGCCGCTT	CGGCCGGCGA	AGAGCTGCC	TGGGGGACGG
670	680	690	700	710	720
ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	CTGGAAGGCG	GTGCTGAGCC
730	740	750	760	770	780
CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	CCAGCTGGTC	CAGGAATAA.

Fig. 30

genome	10	20	30	40	50	
cDNA	1 ATGAAGGCCG	TGGGGCCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	
cDNA	1 ATGAAGGCCG	TGGGGCCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	50
						50
genome	60	70	80	90	100	
cDNA	51 CCTGCAGGGG	GCTGCCAGCA	GAGCCCCACCA	GCACCTCCATG	GAGATCCGCA	
cDNA	51 CCTGCAGGGG	GCTGCCAGCA	GAGCCCCACCA	GCACCTCCATG	GAGATCCGCA	100
						100
genome	110	120	130	140	150	
cDNA	101 GTGAGTGTCT	AGCCCCGCC	CTGCCCCCAG	GGGTCAACAGG	GGGGGCCTGG	
cDNA	101 -----	-----	-----	-----	-----	150
						150
genome	160	170	180	190	200	
cDNA	151 CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA	GCATCCTGGG	GTGGGGTTT	
cDNA	151 -----	-----	-----	-----	-----	200
						200
genome	210	220	230	240	250	
cDNA	201 GGCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCGGA	CAGGTGCTCC	
cDNA	201 -----	-----	-----	-----	-----	250
						250
genome	260	270	280	290	300	
cDNA	251 CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACTCCTC	ACACACACGGG	
cDNA	251 -----	-----	-----	-----	-----	300
						300
genome	310	320	330	340	350	
cDNA	301 TGGCCTGGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	
cDNA	301 -----	-----	-----	-----	-----	350
						350
genome	360	370	380	390	400	
cDNA	351 GGAAAGGAAG	GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	
cDNA	351 -----	-----	-----	-----	-----	400
						400
genome	410	420	430	440	450	
cDNA	401 AAGCCACCCC	AGCACCAAGAA	ATGGGGCCTC	CGGGTGAAAC	TCTGTGGGG	
cDNA	401 -----	-----	-----	-----	-----	450
						450
genome	460	470	480	490	500	
cDNA	451 GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA	GGCAGCCATG	AGCTGAGCAC	
cDNA	451 -----	-----	-----	-----	-----	500
						500
genome	510	520	530	540	550	
cDNA	501 ACACCCGGCC	CGGCCACCAAG	GGCTGTATGC	TCCAGGGCAC	AGGCCTCCAT	
cDNA	501 -----	-----	-----	-----	-----	550
						550
genome	560	570	580	590	600	
cDNA	551 GCGCTCTTCT	CTCTCTTTC	AGCCCCCGAC	ATCAACCTCT	CCTGGTACGC	
cDNA	551 -----	-----	CCCCCGAC	ATCAACCTCT	CCTGGTACGC	600
						600
genome	610	620	630	640	650	
cDNA	601 AGGCCGTGGG	ATCCGGCCCG	TGGGGCGCTT	CGGCCGGCGA	AGAGCTGCC	
cDNA	601 GGGCCGTGGG	ATCCGGCCCG	TGGGGCGCTT	CGGCCGGCGA	AGAGCTGCC	650
						650
genome	660	670	680	690	700	
cDNA	651 TGGGGGACGG	ACCCAGGCCT	GGCCCCCGGC	GTGTGCGGGC	CTGCTTCCGC	
cDNA	651 CGGGGGACGG	ACCCAGGCCT	GGCCCCCGGC	GTGTGCGGGC	CTGCTTCCGC	700
						700
genome	710	720	730	740	750	
cDNA	701 CTGGAAGGCCG	GTGCTGAGCC	CTCCCCGAGCC	CTCCCCGGGC	GGCTGACGGC	
cDNA	701 CTGGAAGGCCG	GTGCTGAGCC	CTCCCCGAGCC	CTCCCCGGGC	GGCTGACGGC	750
						750
genome	760	770	780	790	800	
cDNA	751 CCAGCTGGTC	CAGGAATAA.	
cDNA	751 CCAGCTGGTC	CAGGAATAA.	800
						800

Fig. 31

Fig. 32

1	GGCATCATCCAGGAAGACGGAGCATGGCCCTGAAGACGTGGCTTCTGTGCTGCTGCTG	59
1	MetAlaLeuLysThrTrpLeuLeuCysLeuLeuLeu	12
60	CTAACGCTTGGTCCTCCCAGGGGCTTCCAGCCGAGCCCACCAGCACTCCATGGAGACAAGA	119
13	LeuSerLeuValLeuProGlyAlaSerSerArgAlaHisGlnHisSerMetGluThrArg	32
120	ACCCCTGATATCAATCCTGCCTGGTACACGGGCCGGGATCAGGCCTGTGGGCCGCTTC	179
33	ThrProAspIleAsnProAlaTrpTyrThrGlyArgGlyIleArgProValGlyArgPhe	52
180	GGCAGGGAGAAGGGCAACCCCGAGGGATGTCACTGGACTTGGCCAACTCAGCTGCCTCCCA	239
53	GlyArgArgArgAlaThrProArgAspValThrGlyLeuGlyGlnLeuSerCysLeuPro	72
240	CTGGATGGACGCCACCAAGTTCTCTCAGCGTGGATAAACACCCCCAGCTCGAGAACAGTC	299
73	LeuAspGlyArgThrLysPheSerGlnArgGly***	83
300	TGCTGAGCCCAAGCCCACACTCCCTGTCCCCCTGCAGACCCCTCCTTACCCCTCCCTTCCT	359
83		83
360	CTGCT	364
		83

Fig. 33

bovine.aa		M K A V G A W L L		
bovine.seq	10 20 30 40 50			
rat.seq	-18 GT GGAATGAAGG CGGTGGGGGC CTGGCTCCTC			32
	1 GGCAATCATCC AGGAAGACGG ACCATG---G CCCTGAAGAC <u>GTGGCTTCTG</u>			50
bovine.aa	C L L L L G L A L Q G A A S R A H			
bovine.seq	60 70 80 90 100			
rat.seq	33 TGCTTGCTGC TGCTGGGCCT GGCCTTGAG GGGGCTGCCA GCAGAGCCCCA			82
	51 TGCTTGCTGC TGCTAAGCTT GGTCCTCCCA GGGGCTTCCA GCCGAGCCCCA			100
bovine.aa	R1			
bovine.seq	Q H S M E I R T P D I N P A W Y A			
rat.seq	110 120 130 140 150			
	83 CCAGCACTCC ATGGAGATCC GCACCCCCCGA CATCAACCT GCCTGGTACG			132
	101 CCAGCACTCC ATGGAGACAA GAACCCCTGA TATCAATCCT GCCTGGTACA			150
bovine.aa	R3			
bovine.seq	G R G I R P V G R F G R R R A A			
rat.seq	160 170 180 190 200			
	133 CGGGCCGTGG GATCCGGCCC GTGGGGCGCT TCGGCCCCGG AAGAGCTGCC			182
	151 CGGGCCCGGG GATCAGGGCT GTGGGGCGCT TCGGCAGGAG AAGGGCAACC			200
bovine.aa	R4			
bovine.seq	P G D G P R P G P R R V P A C F R			
rat.seq	210 220 230 240 250			
	183 CCGGGGGACG GACCCAGGCC TGCCCCCGG CGTGCGCCCG CCTGCTTCCG			232
	201 CCGAGGGATG TCACTGGACT TGGC----- ---CACTCA GCTGCCCTCCC			250
bovine.aa				
bovine.seq	L E G G A E P S R A L P G R L T A			
rat.seq	260 270 280 290 300			
	233 CCTGGAAGGC GGGCTGAGC CCTCCCGAGC CCTCCCCGGG CGGCTGACGG			282
	251 ACTGGATGGA CGCACCAAGT TCTCTCAGGG TGGATAACAC CCCAGCTCGA			300
bovine.aa				
bovine.seq	Q L V Q E *			
rat.seq	310 320 330 340 350			
	283 CCCAGCTGGT CCAGGAATAA CAGGGGGAGC CTGCCCCCA CCCCTCTCC			332
	301 GAAGACAGTG CTGCTGAGCC CAAGCCACA CTCCCTGTCC CCTGAGACC			350
bovine.seq	360 370 380 390 400			
rat.seq	333 TCCACCAGCC ACCTTCCCTC CAGTCCTAAT AAAAGCAGCT GGCTTGT..			382
	351 CTCCCTCTACC CTCCCTCTCC TCTGCT....			400

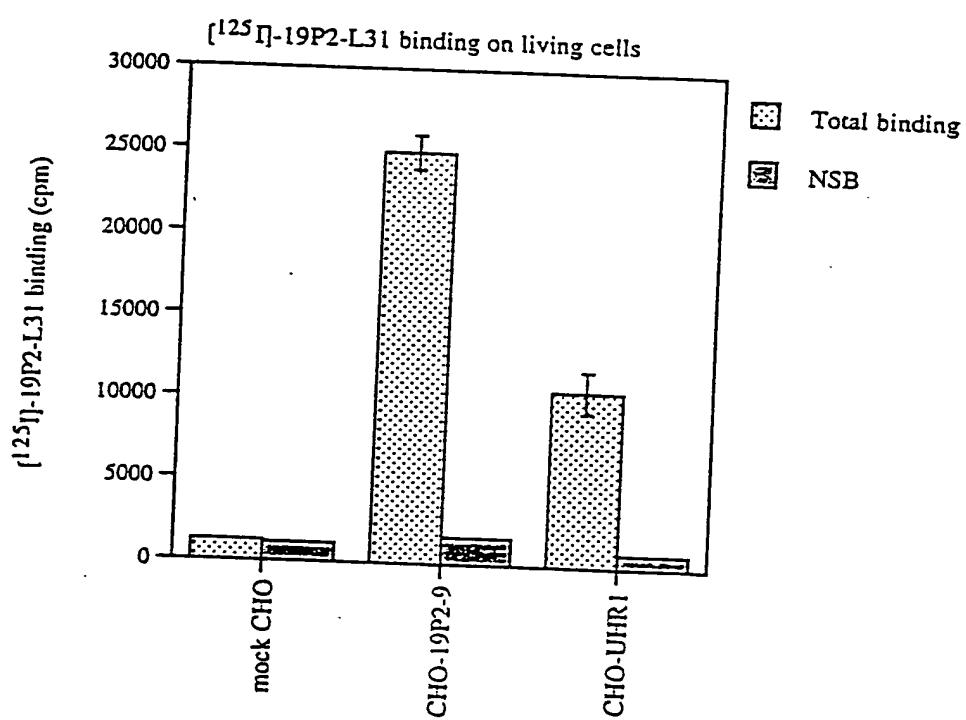
Fig. 34

1	GGCCTCCTCGGAGGAGCCAAGGGATGAAGGTGCTGAGGGCCTGGCTCCTGTGCCTGCTG	59
1	MetLysValLeuArgAlaTrpLeuLeuCysLeuLeu	12
60	ATGCTGGGCCTGGCCCTGCGGGGAGCTGCAAGTCGTACCCATCGGCACTCCATGGAGATC	119
13	MetLeuGlyLeuAlaLeuArgGlyAlaAlaSerArgThrHisArgHisSerMetGluIle	32
120	CGCACCCCTGACATCAATCCTGCCTGGTACGCCAGTCGCGGGATCAGGCCTGTGGGCCGC	179
33	ArgThrProAspIleAsnProAlaTrpTyrAlaSerArgGlyIleArgProValGlyArg	52
180	TTCGGTCGGAGGAGGGCAACCCTGGGGGACGTCCCCAAGCCTGGCCTGCGACCCCCGGCTG	239
53	PheGlyArgArgAlaThrLeuGlyAspValProLysProGlyLeuArgProArgLeu	72
240	ACCTGCTTCCCCCTGGAAGGCAGGTGCTATGTCGTCCCAGGATGGCTGACAGCCAGCTTGT	299
73	ThrCysPheProLeuGluGlyGlyAlaMetSerSerGlnAspGly***	87
300	CAAGAAACTCACTCTGGAGCCTCCCCACCCCACCCCTCTCCTCTCGGGCTCCTTTC	359
87		87
360	CC	361
87		87

Fig. 35

bovine.aa	1	MKAVGAWLLC	10	20	30	40	50	
rat.aa	1	M-ALKTWLIC	10	20	30	40	50	50
human.aa	1	MKVLRRAWLLC	10	20	30	40	50	50
bovine.aa	51	GRFGRRRAAP	60	70	80	90	100	
rat.aa	51	GRFGRRRATP	60	70	80	90	100	100
human.aa	51	GRFGRRRAIL	60	70	80	90	100	100

Fig. 36



cells; 0.5×10^7 cells/ml
 $[^{125}\text{I}]$ -19P2-L31; 200pM (avg. 63857.3 cpm)
 NSB; 200nM ($\times 1,000$)
 reaction; RT, 2.5hr
 in HBSS + 0.05% BSA + 0.05% CHAPS
 in 100 μl

Fig. 37

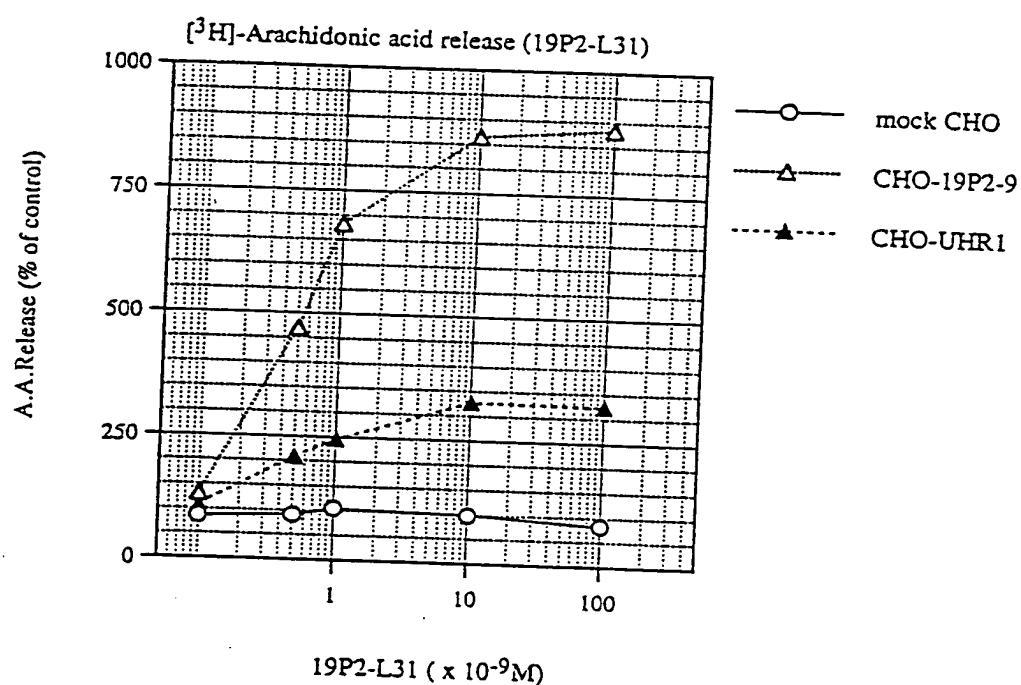


Fig. 38

UHR-1

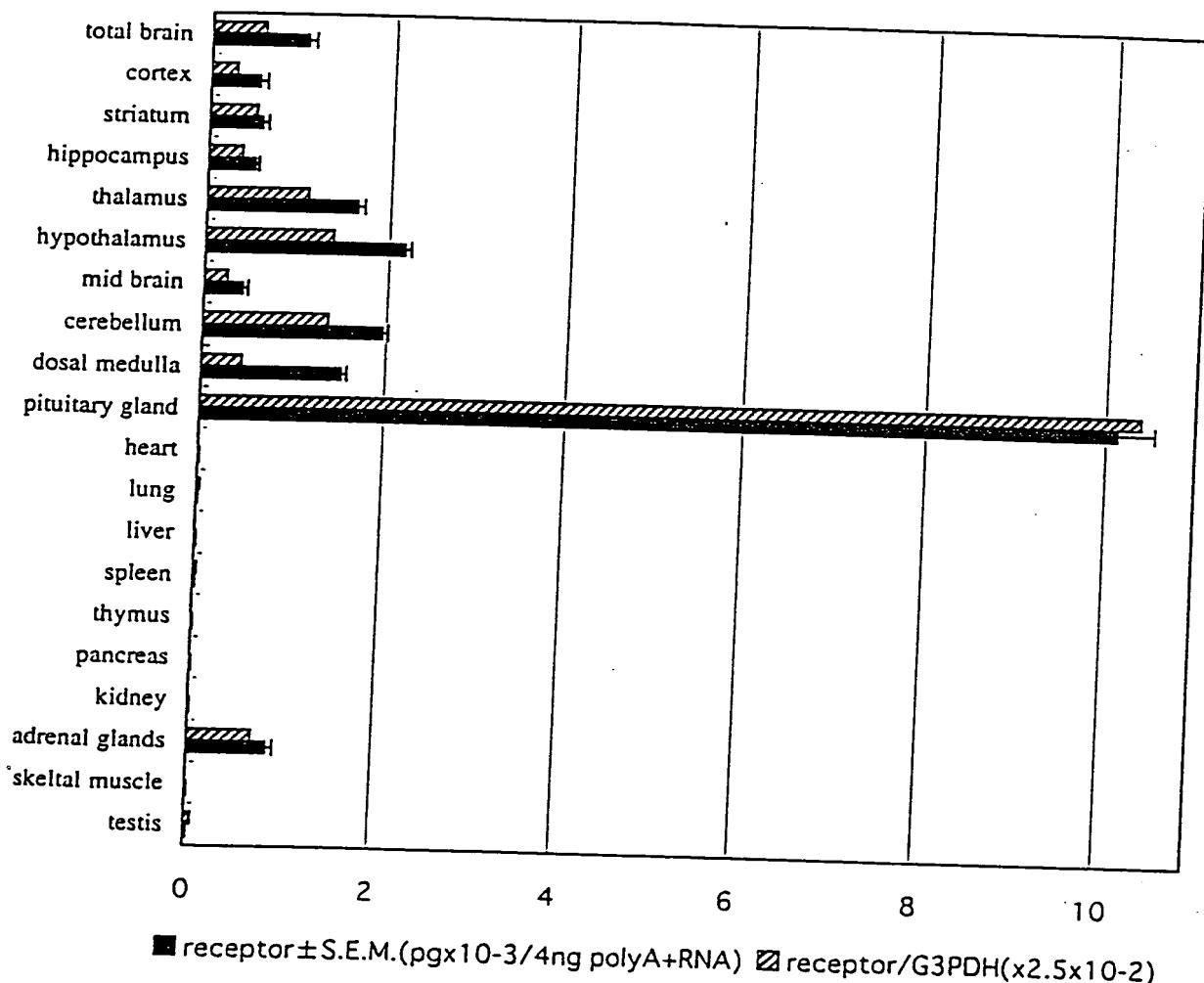


Fig. 39

ligand polypeptide

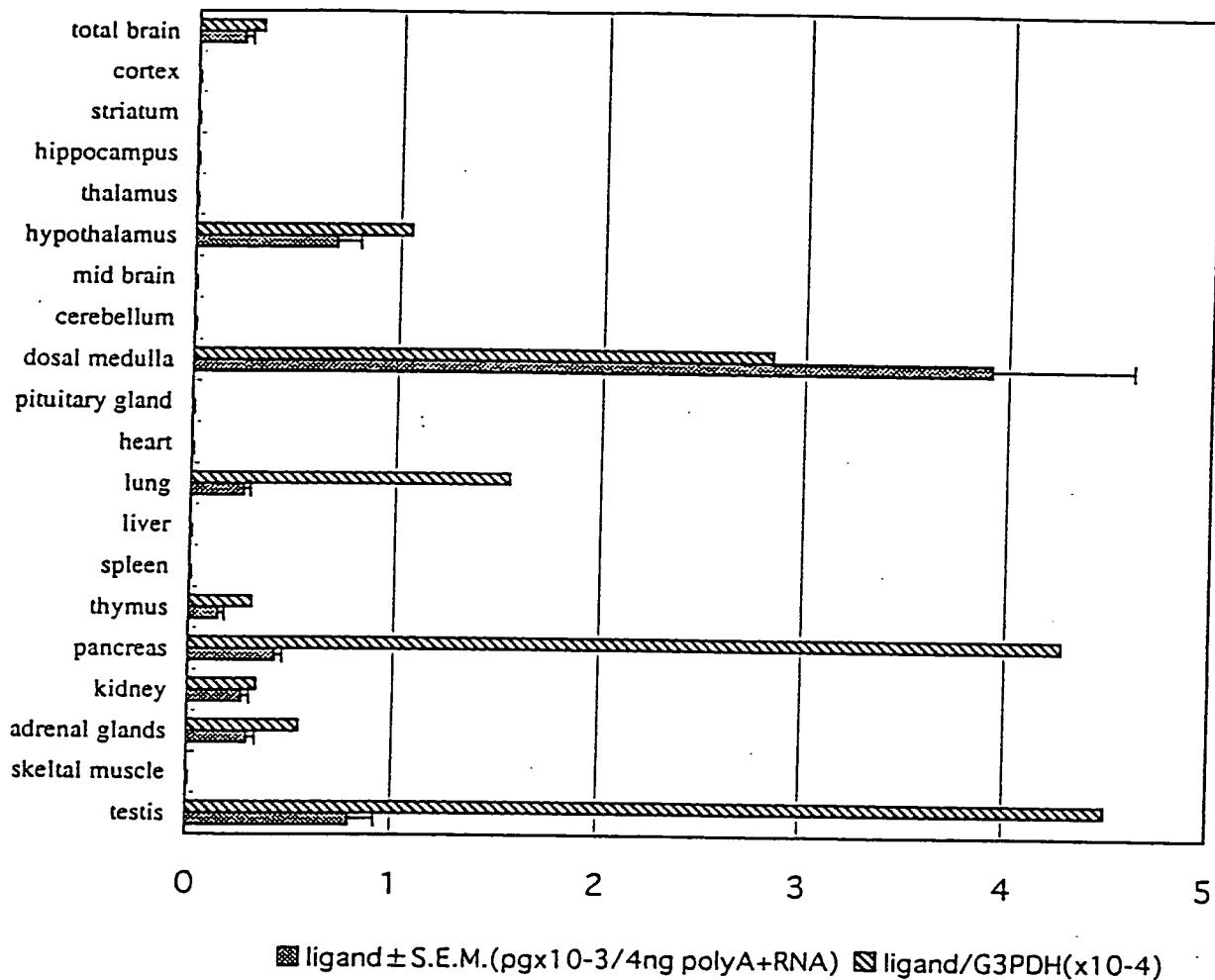


Fig. 40

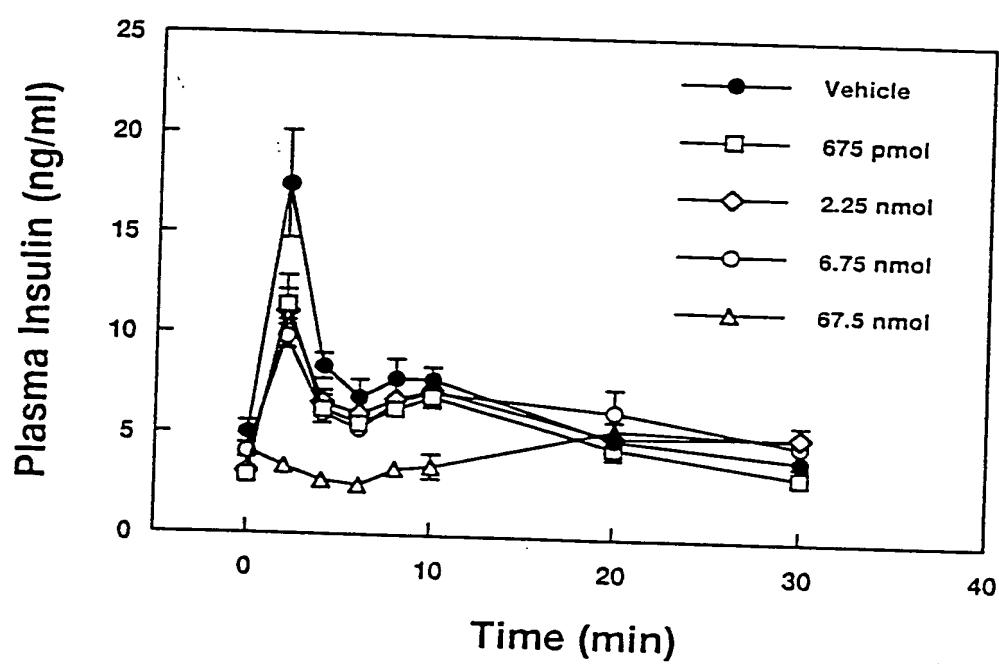
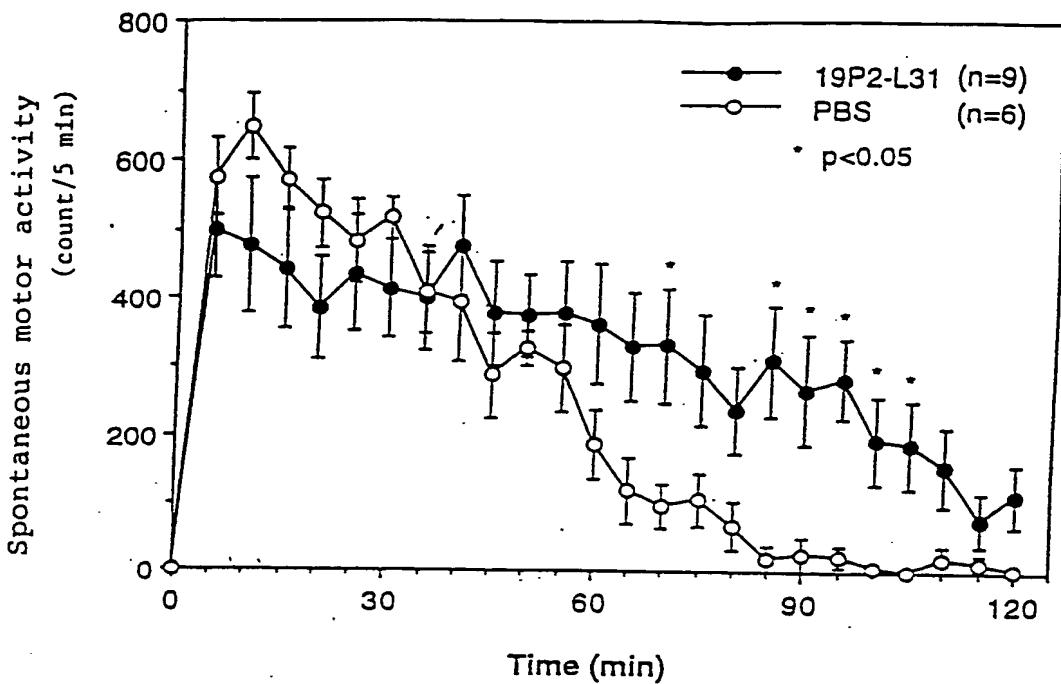


Fig. 41

(a)



(b)

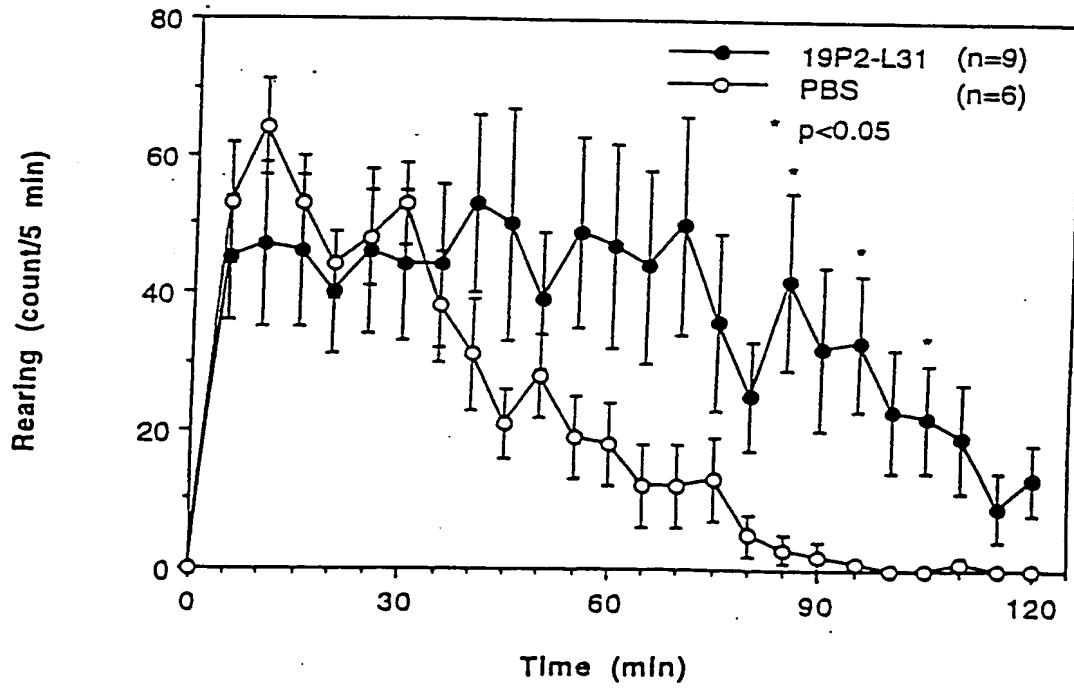
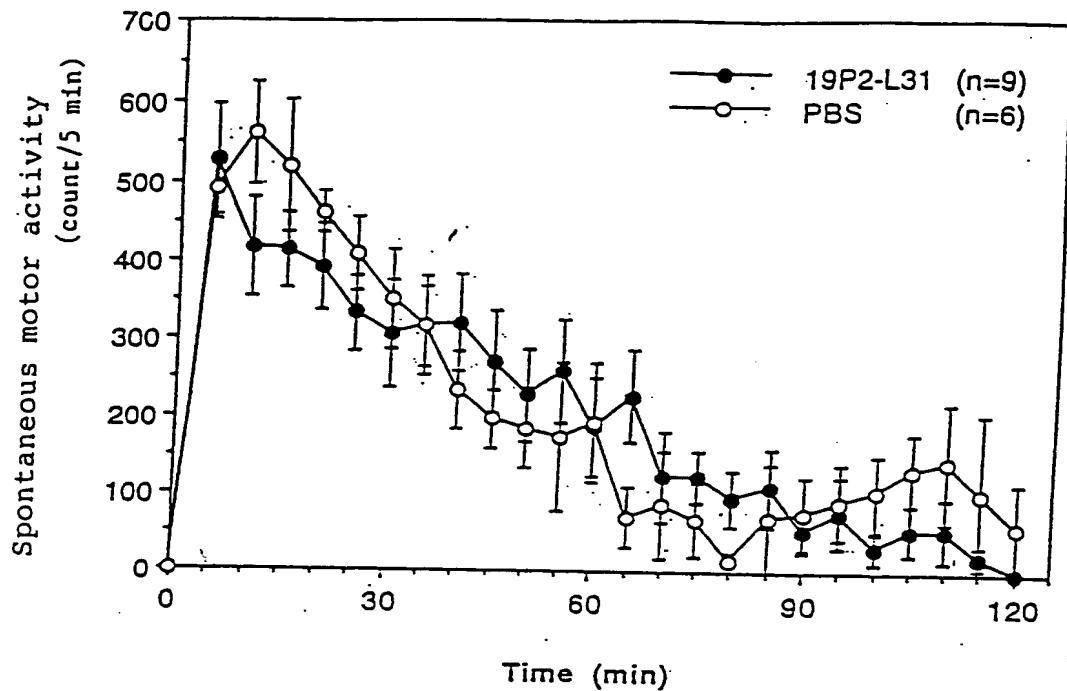


Fig. 42

(a)



(b)

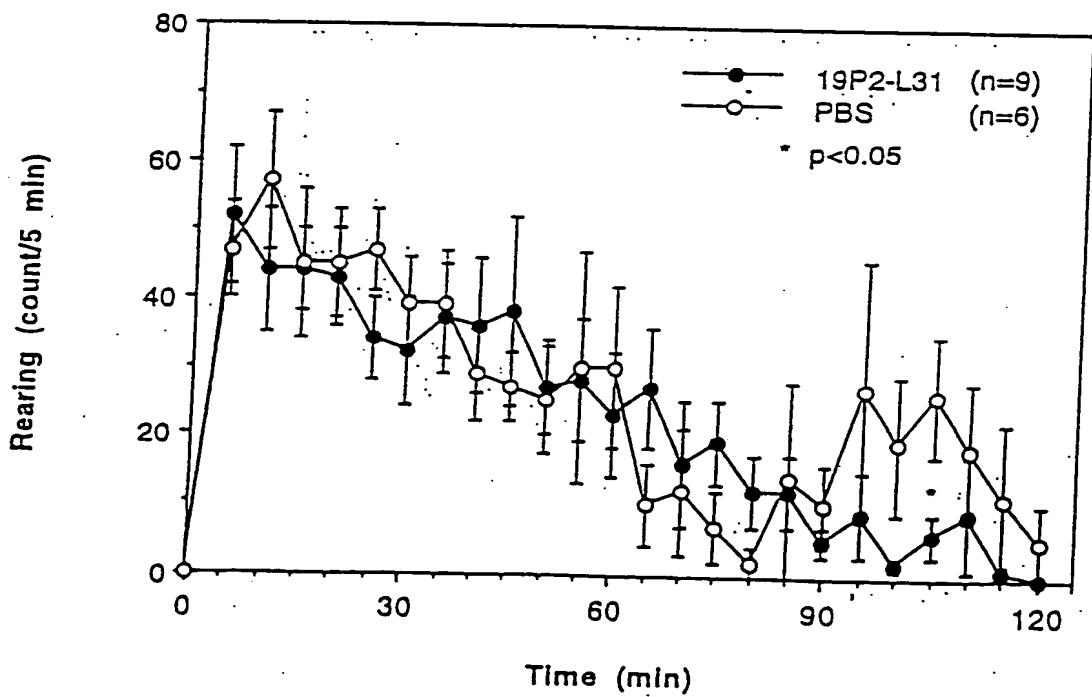
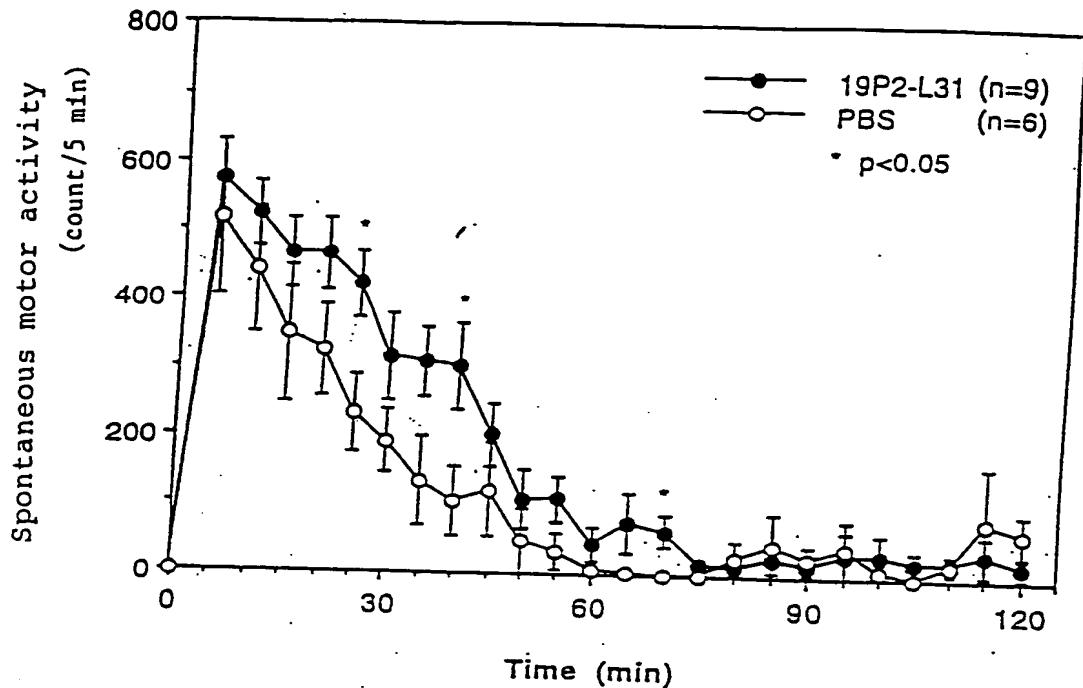


Fig. 43

(a)

 $p < 0.05$

(b)

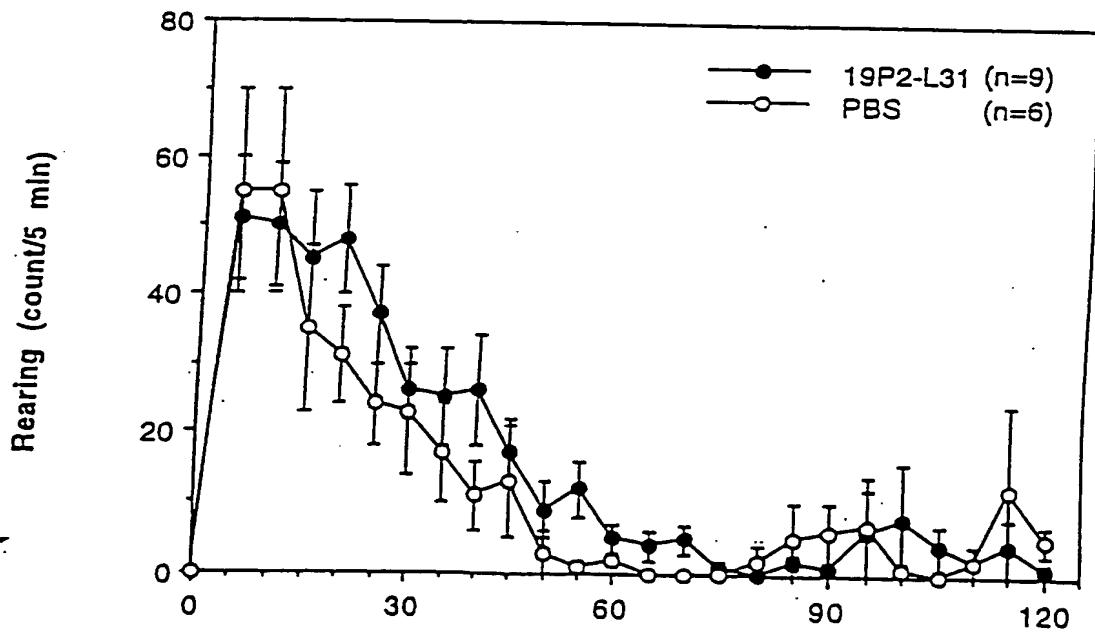
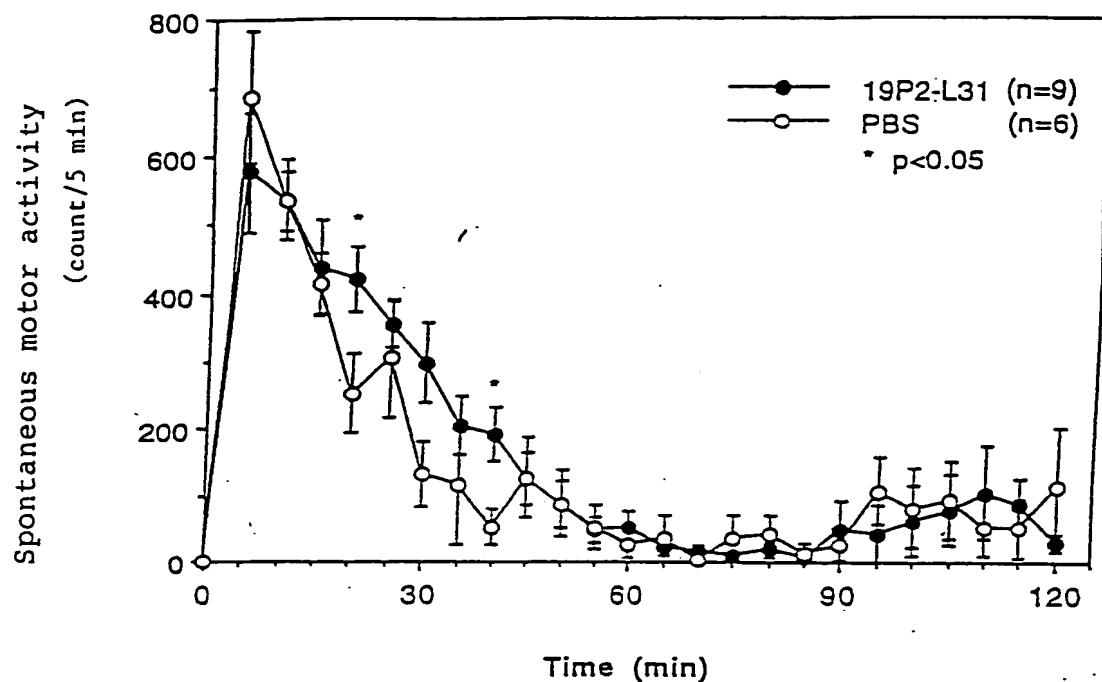


Fig. 44

(a)



(b)

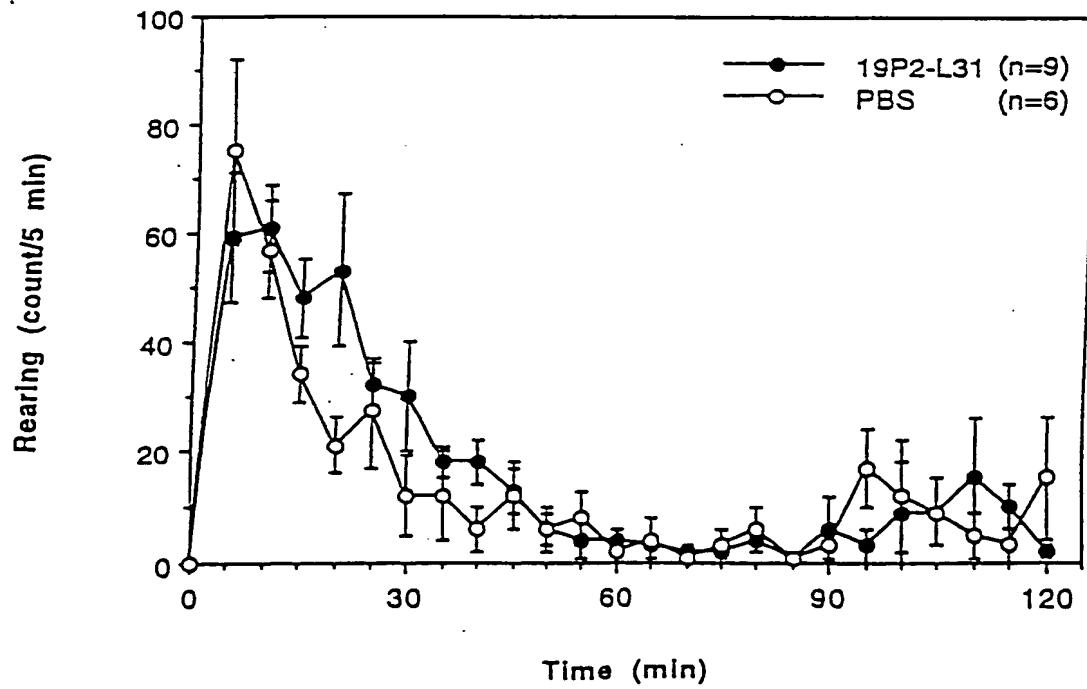


Fig. 45

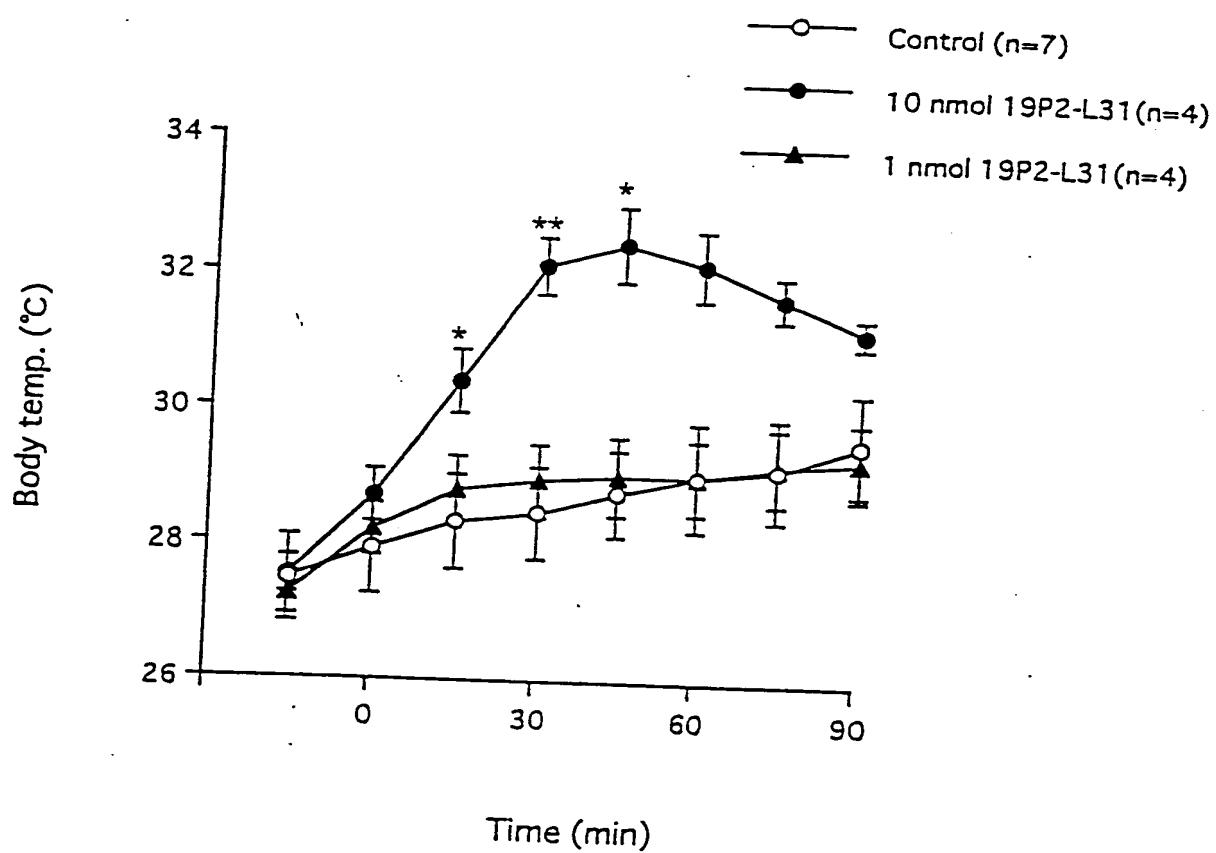
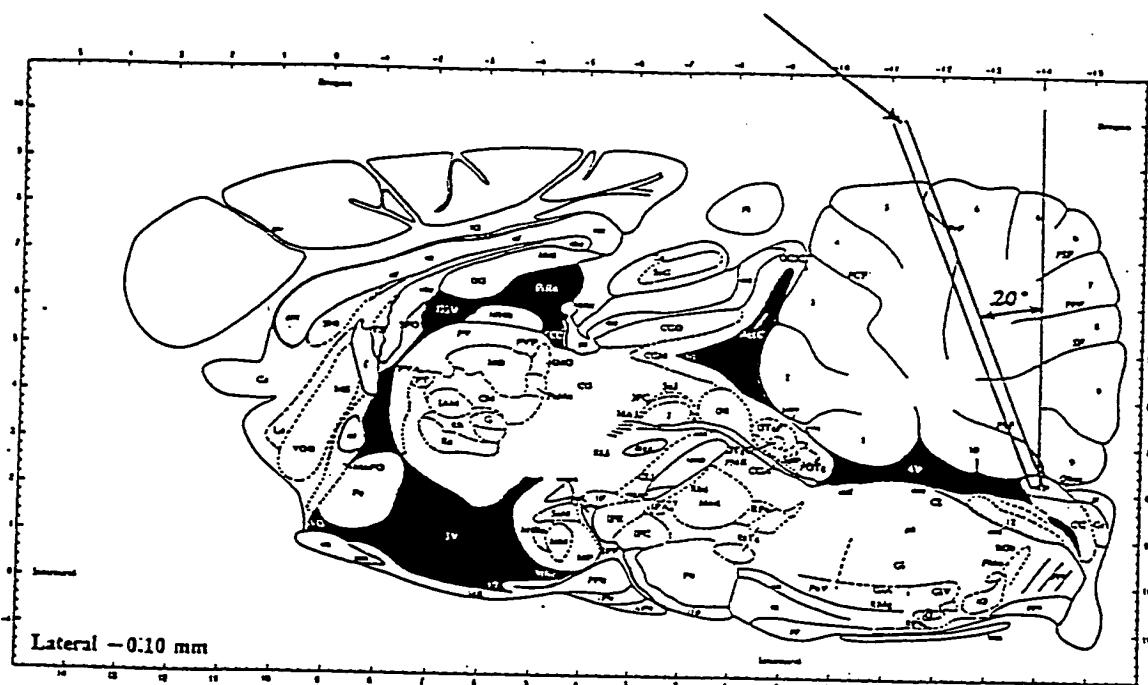
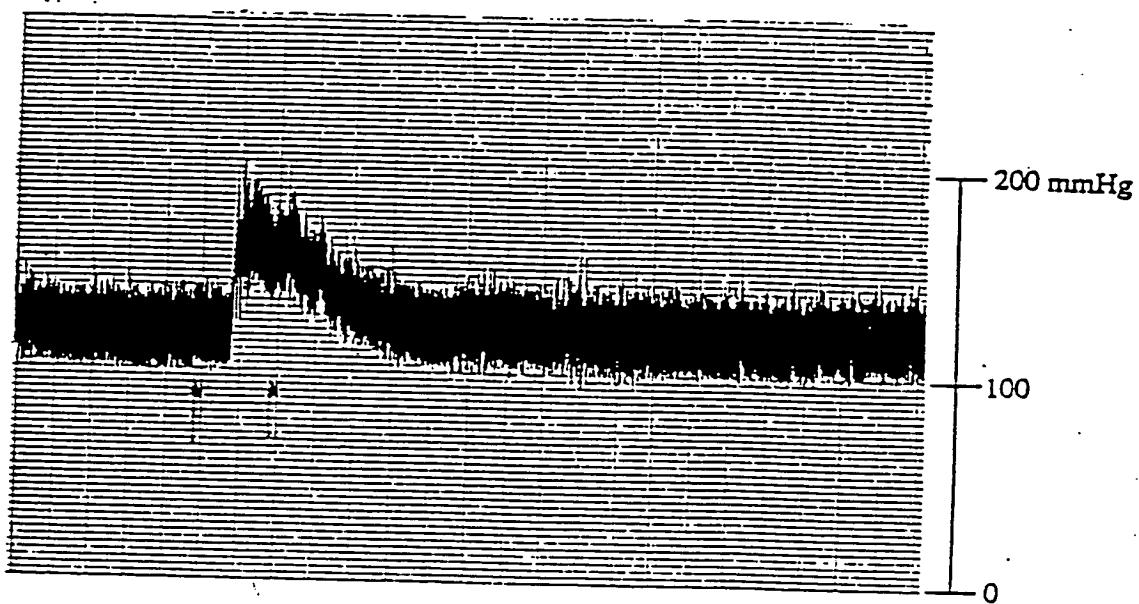


Fig. 46

micro-injection cannula



direct blood pressure



mean blood pressure

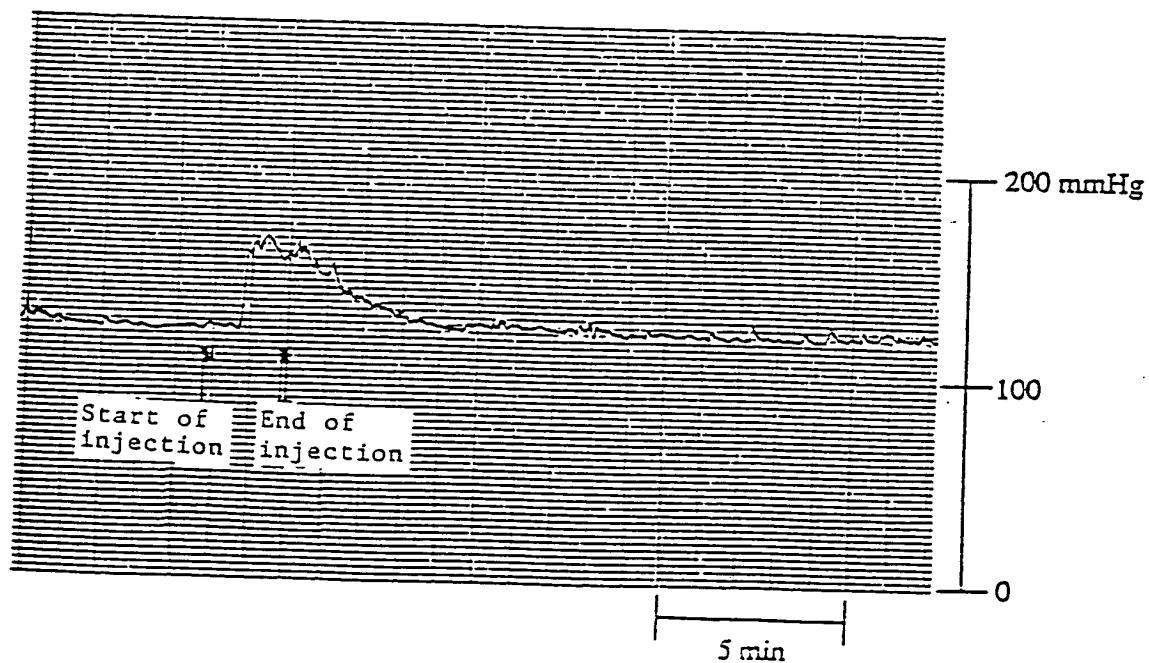


Fig. 48

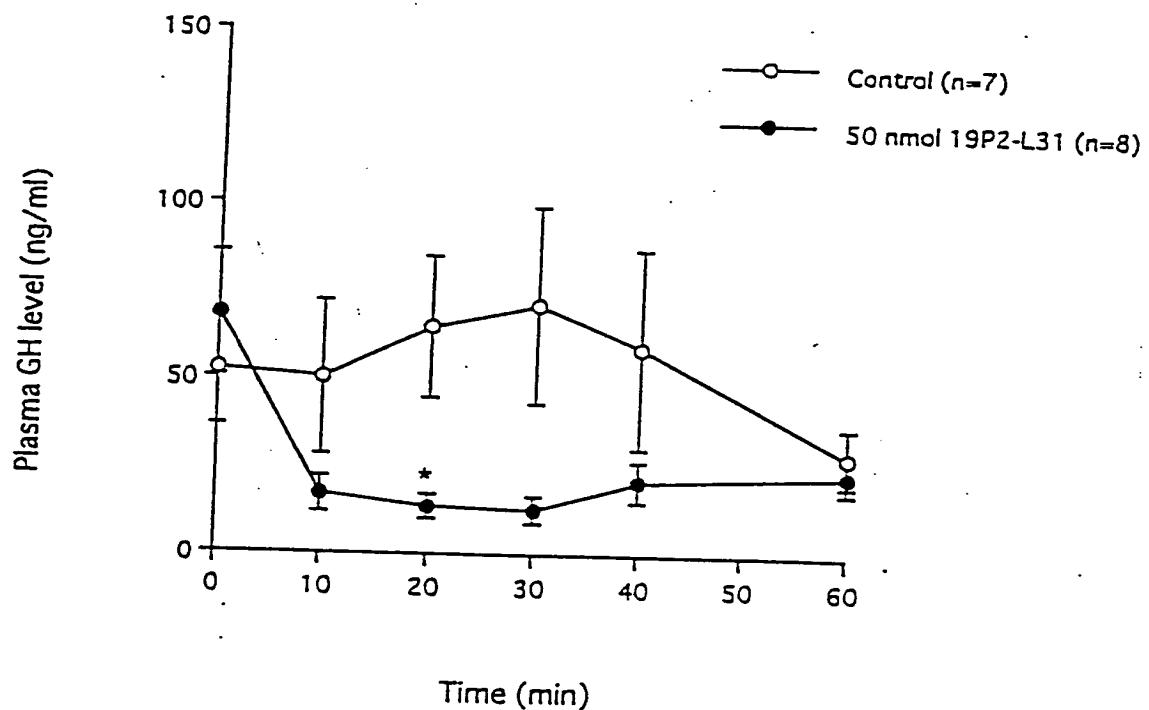


Fig. 49

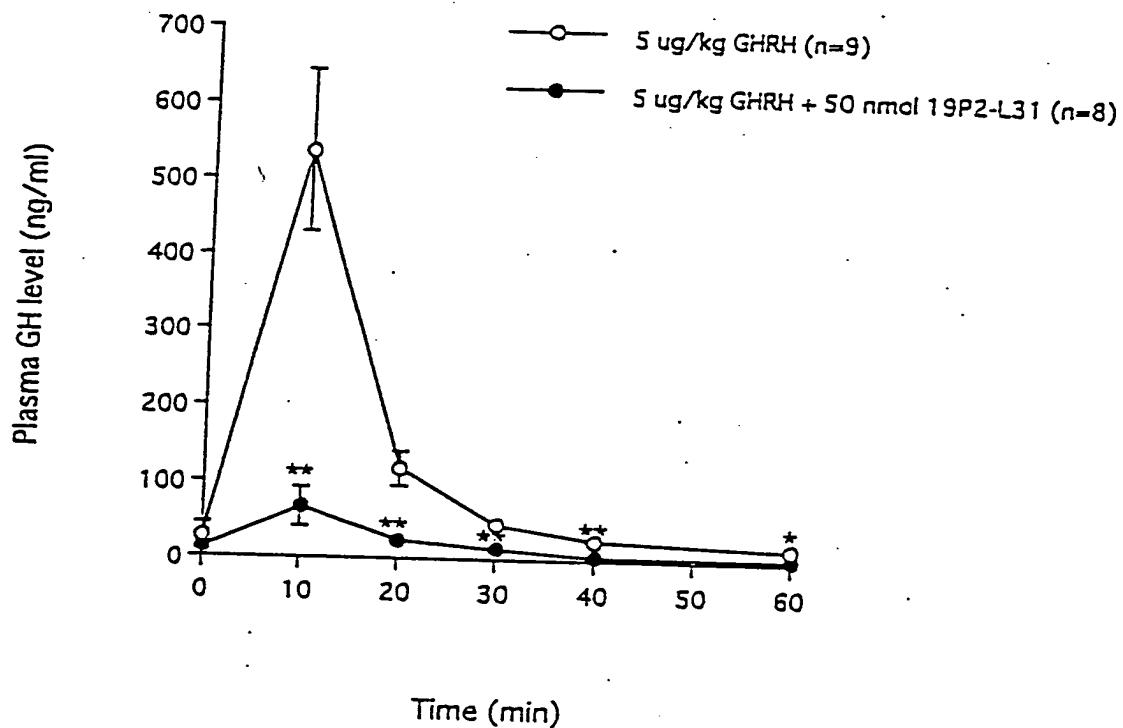


Fig. 50

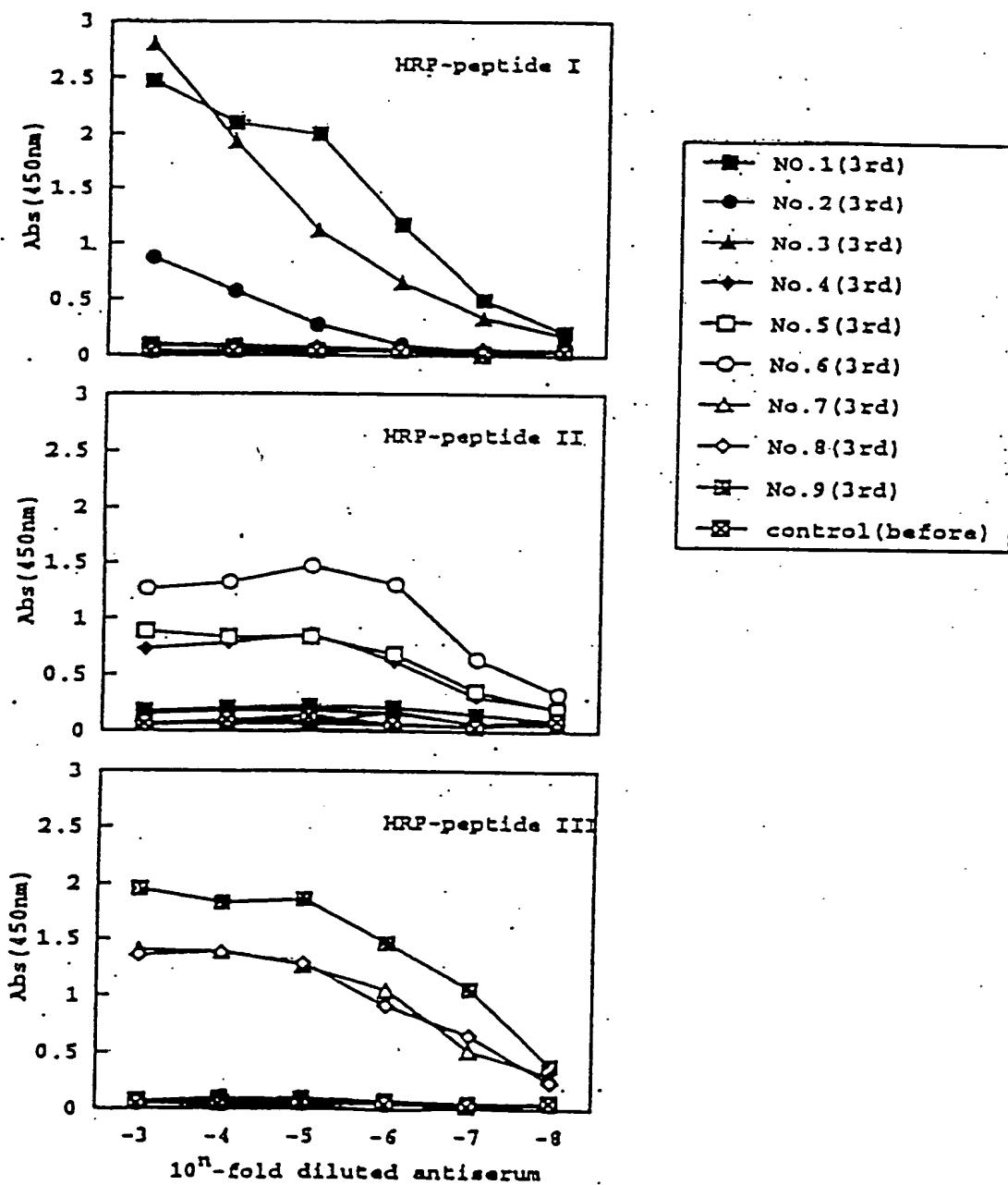


Fig. 51

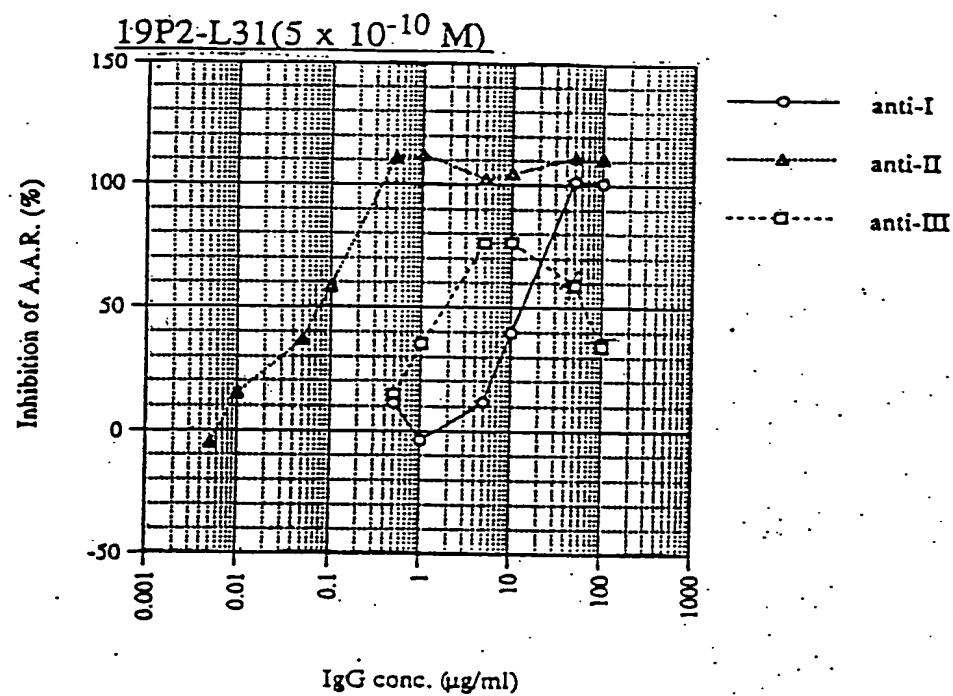


Fig. 52

5' ATG ACT TGA TGC CCT GCA ACT ACT GCG CAC CCC CAT TTG TTT TCT CCT CGG 18
 Met Thr Ser Leu Pro Pro Gly Thr Thr Gly Arg Pro Arg Leu Phe Ser Gly Pro
 TCC GCA CCT GCG TCC ACT GCA CCT AAC CAG ACT GCA CAG CCT TCA CAG ACC AAT
 Ser Pro Ala Gly Ser Thr Pro Ala Asn Glu Ser Ala Glu Ala Ser Glu Ser Asn
 GTC CCT CCT CCT CCT GCA CCT GCA GTC ACC CCT CCT TTG CAG ACC GTC GCA
 Val Ser Ala Thr Val Pro Arg Ala Ala Val Thr Pro Phe Cln Ser Leu Cln
 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 399 400 401 402 403 404 405 406 407 408 409 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 499 500 501 502 503 504 505 506 507 508 509 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 529 530 531 532 533 534 535 536 537 538 539 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 559 560 561 562 563 564 565 566 567 568 569 569 570 571 572 573 574 575 576 577 578 579 579 580 581 582 583 584 585 586 587 588 589 589 590 591 592 593 594 595 596 597 598 599 599 600 601 602 603 604 605 606 607 608 609 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 659 660 661 662 663 664 665 666 667 668 669 669 670 671 672 673 674 675 676 677 678 679 679 680 681 682 683 684 685 686 687 688 689 689 690 691 692 693 694 695 696 697 698 699 699 700 701 702 703 704 705 706 707 708 709 709 710 711 712 713 714 715 716 717 718 719 719 720 721 722 723 724 725 726 727 728 729 729 730 731 732 733 734 735 736 737 738 739 739 740 741 742 743 744 745 746 747 748 749 749 750 751 752 753 754 755 756 757 758 759 759 760 761 762 763 764 765 766 767 768 769 769 770 771 772 773 774 775 776 777 778 779 779 780 781 782 783 784 785 786 787 788 789 789 790 791 792 793 794 795 796 797 798 799 799 800 801 802 803 804 805 806 807 808 809 809 810 811 812 813 814 815 816 817 818 819 819 820 821 822 823 824 825 826 827 828 829 829 830 831 832 833 834 835 836 837 838 839 839 840 841 842 843 844 845 846 847 848 849 849 850 851 852 853 854 855 856 857 858 859 859 860 861 862 863 864 865 866 867 868 869 869 870 871 872 873 874 875 876 877 878 879 879 880 881 882 883 884 885 886 887 888 889 889 890 891 892 893 894 895 896 897 898 899 899 900 901 902 903 904 905 906 907 908 909 909 910 911 912 913 914 915 916 917 918 919 919 920 921 922 923 924 925 926 927 928 929 929 930 931 932 933 934 935 936 937 938 939 939 940 941 942 943 944 945 946 947 948 949 949 950 951 952 953 954 955 956 957 958 959 959 960 961 962 963 964 965 966 967 968 969 969 970 971 972 973 974 975 976 977 978 979 979 980 981 982 983 984 985 986 987 988 989 989 990 991 992 993 994 995 996 997 998 999 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1989 1990 1991 1992 1993 1994 1995 1996 1997 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